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OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 22:21:22 ; Search time 128 Seconds  
(without alignments)  
255.668 Million cell updates/sec

Title: US-10-643-801A-35

Perfect score: 20  
Sequence: 1 gcatgcctaccctccatctc 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 8

Total number of hits satisfying chosen parameters: 153720

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/6C\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/6D\_COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	827	US-10-121-857-56	Sequence 56, Appl
2	20	100.0	885	US-10-121-857-60	Sequence 60, Appl
3	20	100.0	2519	US-10-121-757B-7	Sequence 7, Appl
4	16	80.0	616	US-09-854-133-666	Sequence 666, Appl
5	15	75.0	508	US-09-621-976-1551	Sequence 1551, Appl
6	15	75.0	601	US-09-949-016-43149	Sequence 43149, A
7	15	75.0	601	US-09-949-016-43378	Sequence 43378, A
8	15	75.0	601	US-09-949-016-43607	Sequence 43607, A
9	15	75.0	601	US-09-949-016-117164	Sequence 117164, A
10	15	75.0	1479	US-09-583-110-1385	Sequence 1385, Appl
11	15	75.0	1533	US-09-107-433-545	Sequence 545, Appl
12	15	75.0	11303	US-08-961-527-115	Sequence 115, Appl
13	15	75.0	80717	US-09-949-016-14968	Sequence 14968, A
14	15	75.0	89716	US-09-949-016-11900	Sequence 11900, A
15	15	75.0	157866	US-09-949-016-12982	Sequence 12982, A
16	15	75.0	157866	US-09-949-016-12983	Sequence 12983, A
17	15	75.0	157866	US-09-949-016-12984	Sequence 12984, A
18	15	75.0	265038	US-09-949-016-15779	Sequence 15779, A
19	14	70.0	272	US-09-513-999C-33158	Sequence 33158, A
20	14	70.0	601	US-09-949-016-82921	Sequence 82921, A
21	14	70.0	601	US-09-949-016-82922	Sequence 82922, A
22	14	70.0	601	US-09-949-016-132819	Sequence 132819, A
23	14	70.0	601	US-09-949-016-202121	Sequence 202121, A
24	14	70.0	618	US-09-540-236-1580	Sequence 1580, Appl
25	14	70.0	751	US-09-687-698-14	Sequence 14, Appl
26	14	70.0	751	US-09-705-621-30	Sequence 30, Appl
27	14	70.0	7417	US-09-573-080A-424	Sequence 424, Appl

C 28	14	70.0	7447	US-09-949-016-16540	Sequence 16540, A
C 29	14	70.0	14551	US-09-949-016-12313	Sequence 12313, A
C 30	14	70.0	14551	US-09-949-016-16465	Sequence 16465, A
C 31	14	70.0	21535	US-09-949-016-12826	Sequence 12826, A
C 32	14	70.0	21535	US-09-949-016-12827	Sequence 12827, A
C 33	14	70.0	21535	US-09-949-016-12828	Sequence 12828, A
C 34	14	70.0	21535	US-09-949-016-12829	Sequence 12829, A
C 35	14	70.0	21536	US-09-949-016-13366	Sequence 13366, A
C 36	14	70.0	21536	US-09-949-016-13367	Sequence 13367, A
C 37	14	70.0	21536	US-09-949-016-13368	Sequence 13368, A
C 38	14	70.0	21536	US-09-949-016-13369	Sequence 13369, A
C 39	14	70.0	34279	US-09-556-002-26	Sequence 26, Appl
C 40	14	70.0	36544	US-09-949-016-12149	Sequence 12149, A
C 41	14	70.0	47818	US-09-949-016-12374	Sequence 12374, A
C 42	14	70.0	47818	US-09-949-016-12375	Sequence 12375, A
C 43	14	70.0	48480	US-09-949-016-12500	Sequence 12500, A
C 44	14	70.0	53336	US-09-949-016-15166	Sequence 15166, A
C 45	14	70.0	53337	US-09-949-016-16032	Sequence 16032, A
C 46	14	70.0	53337	US-09-949-016-16032	Sequence 16032, A
C 47	14	70.0	97196	US-09-949-016-16971	Sequence 16971, A
C 48	14	70.0	99580	US-09-949-016-17411	Sequence 17411, A
C 49	14	70.0	194714	US-09-949-016-15474	Sequence 15474, A
C 50	14	70.0	196714	US-09-820-007-3	Sequence 3, Appl
C 51	14	70.0	213456	US-09-949-016-13113	Sequence 13113, A
C 52	14	70.0	246444	US-09-949-016-14139	Sequence 14139, A
C 53	14	70.0	323820	US-08-916-421B-1	Sequence 1, Appl
C 54	14	70.0	1664976	US-09-692-570-1	Sequence 2606, Appl
C 55	14	70.0	1664976	US-08-956-171E-2606	Sequence 2606, Appl
C 56	13	65.0	54	US-08-781-986A-2606	Sequence 138, Appl
C 57	13	65.0	178	US-08-036-555B-138	Sequence 138, Appl
C 58	13	65.0	178	US-08-469-569-138	Sequence 138, Appl
C 59	13	65.0	178	US-08-249-322A-138	Sequence 138, Appl
C 60	13	65.0	178	US-08-469-526A-138	Sequence 138, Appl
C 61	13	65.0	178	US-08-734-91A-138	Sequence 138, Appl
C 62	13	65.0	178	US-08-469-660-138	Sequence 13, Appl
C 63	13	65.0	178	US-08-341-018-13	Sequence 138, Appl
C 64	13	65.0	178	US-08-470-335-138	Sequence 138, Appl
C 65	13	65.0	178	US-08-735-021-138	Sequence 138, Appl
C 66	13	65.0	178	US-08-734-664A-138	Sequence 138, Appl
C 67	13	65.0	178	US-08-470-339-138	Sequence 138, Appl
C 68	13	65.0	178	US-08-467-602-138	Sequence 12, Appl
C 69	13	65.0	178	US-08-411-295F-12	Sequence 134, Appl
C 70	13	65.0	178	PCT-US94-05083C-134	Sequence 138, Appl
C 71	13	65.0	178	PCT-US95-06846A-138	Sequence 70, Appl
C 72	13	65.0	287	US-09-985-799-70	Sequence 70, Appl
C 73	13	65.0	287	US-09-977-371-70	Sequence 70, Appl
C 74	13	65.0	287	US-08-594-031-70	Sequence 189, Appl
C 75	13	65.0	400	US-08-956-171B-1989	Sequence 189, Appl
C 76	13	65.0	400	US-08-781-986A-1989	Sequence 131, Appl
C 77	13	65.0	400	US-08-615-192A-131	Sequence 131, Appl
C 78	13	65.0	478	US-09-169-789-131	Sequence 13149, A
C 79	13	65.0	478	US-09-621-976-13514	Sequence 13514, A
C 80	13	65.0	483	US-09-621-976-13514	Sequence 13514, A
C 81	13	65.0	490	US-09-621-976-13514	Sequence 63, Appl
C 82	13	65.0	492	US-08-975-316-63	Sequence 63, Appl
C 83	13	65.0	492	US-09-615-192A-63	Sequence 219, Appl
C 84	13	65.0	492	US-09-159-789-63	Sequence 15501, A
C 85	13	65.0	572	US-09-270-767-219	Sequence 15514, A
C 86	13	65.0	572	US-09-949-016-15144	Sequence 45144, A
C 87	13	65.0	601	US-09-949-016-15144	Sequence 45144, A
C 88	13	65.0	601	US-09-949-016-15145	Sequence 66326, A
C 89	13	65.0	601	US-09-949-016-66326	Sequence 66326, A
C 90	13	65.0	601	US-09-949-016-66940	Sequence 70882, A
C 91	13	65.0	601	US-09-949-016-70882	Sequence 84085, A
C 92	13	65.0	601	US-09-949-016-84085	Sequence 86882, A
C 93	13	65.0	601	US-09-949-016-86882	Sequence 127701, A
C 94	13	65.0	601	US-09-949-016-127701	Sequence 127701, A
C 95	13	65.0	601	US-09-949-016-127702	Sequence 128039, A
C 96	13	65.0	601	US-09-949-016-128039	Sequence 128039, A
C 97	13	65.0	601	US-09-949-016-128039	Sequence 128039, A
C 98	13	65.0	601	US-09-949-016-157982	Sequence 157982, A
C 99	13	65.0	601	US-09-949-016-157983	Sequence 157983, A
C 100	13	65.0	601	US-09-949-016-157984	Sequence 157984, A

## ALIGNMENTS

## RESULT 1

US-10-121-857-56/c  
; Sequence 56, Application US/10121857  
; Patent No. 6822141  
; GENERAL INFORMATION:  
; APPLICANT: Lardizabal, Kathryn D  
; APPLICANT: Hawkins, Deborah J  
; APPLICANT: Thompson, Gregory A  
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins  
; FILE REFERENCE: 16515.143  
; CURRENT APPLICATION NUMBER: US/10/121,857  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 09/345,461  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,631  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/130,829  
; PRIOR FILING DATE: 1998-04-23  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 827  
; TYPE: DNA  
; ORGANISM: Human  
US-10-121-857-56

Query Match 100.0%; Score 20; DB 4; Length 827;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20

Db 479 GCATTGCCACTCCCATTTCTT 460

## RESULT 2

US-10-121-857-60/c  
; Sequence 60, Application US/10121857  
; Patent No. 6822141  
; GENERAL INFORMATION:  
; APPLICANT: Lardizabal, Kathryn D  
; APPLICANT: Hawkins, Deborah J  
; APPLICANT: Thompson, Gregory A  
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins  
; FILE REFERENCE: 16515.143  
; CURRENT APPLICATION NUMBER: US/10/121,857  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 09/345,461  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,631  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/130,829  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: murine  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(885)  
; OTHER INFORMATION: unsure at all n locations  
US-10-121-857-60

Query Match 100.0%; Score 20; DB 4; Length 885;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
Db 482 GCATTGCCACTCCCATTTCTT 463

## RESULT 3

US-10-121-757B-7/c  
; Sequence 7, Application US/10121757B  
; Patent No. 6835556  
; GENERAL INFORMATION:  
; APPLICANT: Atersand, Anneli  
; TITLE OF INVENTION: Protein Cluster V  
; FILE REFERENCE: 10806-164  
; CURRENT APPLICATION NUMBER: US/10/121,757B  
; CURRENT FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Version 3.1  
; SEQ ID NO 7  
; LENGTH: 2519  
; TYPE: DNA  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (714)..(1373)  
; OTHER INFORMATION:  
US-10-121-757B-7

Query Match 100.0%; Score 20; DB 4; Length 2519;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20

Db 904 GCATTGCCACTCCCATTTCTT 885

## RESULT 4

US-09-854-133-666/c  
; Sequence 666, Application US/09854133  
; Patent No. 6759508  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Mohamath, Raodoh  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.475C10  
; CURRENT APPLICATION NUMBER: US/09/854,133  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 735  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 666  
; LENGTH: 616  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-854-133-666

Query Match 80.0%; Score 16; DB 4; Length 616;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCCACTCCCATTC 18

Db 601 ATTGCCACTCCCATTC 586

## RESULT 5

US-09-621-976-1551/c  
; Sequence 1551, Application US/09621976  
; Patent No. 6639063

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; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTE and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1551
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..360
; NAME/KEY: s1g_peptide
; LOCATION: 43..144
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 6.1998980926514
; OTHER INFORMATION: seq LCLMTGBCAPVVG/SP
US-09-621-976-1551

Query Match          75.0%; Score 15; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TGGCACTCCCATTTCT 19
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Db      313 TGGCACTCCCATTTCT 299

RESULT 6
US-09-949-016-43149/c
; Sequence 43149, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43149
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-43149

Query Match          75.0%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TGGCACTCCCATTTCT 19
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Db      578 TGGCACTCCCATTTCT 564

RESULT 7
US-09-949-016-43378/c
; Sequence 43378, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43378
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-43378

Query Match          75.0%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TGGCACTCCCATTTCT 19
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Db      578 TGGCACTCCCATTTCT 564

RESULT 8
US-09-949-016-43607/c
; Sequence 43607, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43607
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-43607

Query Match          75.0%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TGGCACTCCCATTTCT 19
        |||||
Db      578 TGGCACTCCCATTTCT 564

RESULT 9
US-09-949-016-117164/c
; Sequence 117164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117164
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-117164

Query Match          75.0%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCCACTCCCAT 17
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Db 95 ATTGCCACTCCCAT 81

RESULT 10
US-09-583-110-1385/c
; Sequence 1385, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1385
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1385

Query Match          75.0%; Score 15; DB 4; Length 1479;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCATTC 18
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Db 1092 TTGCCACTCCCATTC 1078

RESULT 11
US-09-107-433-545/c
; Sequence 545, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 545:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1533 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1533
; SEQUENCE DESCRIPTION: SEQ ID NO: 545:
US-09-107-433-545

Query Match          75.0%; Score 15; DB 4; Length 1533;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCATTC 18
   |||||
Db 1146 TTGCCACTCCCATTC 1132

RESULT 12
US-08-961-527-115
; Sequence 115, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
```



```

; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-961-527-115

Query Match          75.0%; Score 15; DB 3; Length 11303;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      4 TTGCGACTCCCATTC 18
Db      9199 TTGCGACTCCCATTC 9213

RESULT 13
US-09-949-016-14968
; Sequence 14968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14968
; LENGTH: 80717
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(80717)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-949-016-14968

Query Match          75.0%; Score 15; DB 4; Length 80717;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      3 ATTGCGACTCCCATTC 17
Db      35880 ATTGCGACTCCCATTC 35894

RESULT 14
US-09-949-016-11900/C
; Sequence 11900, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
```

```

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11900
; LENGTH: 89716
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(89716)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-949-016-11900

Query Match          75.0%; Score 15; DB 4; Length 89716;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 TGGCACTCCCATTCCT 19
Db      13066 TGGCACTCCCATTCCT 13052

RESULT 15
US-09-949-016-12982
; Sequence 12982, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12982
; LENGTH: 157866
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-12982

Query Match          75.0%; Score 15; DB 4; Length 157866;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 TGGCACTCCCATTCCT 19
Db      16979 TGGCACTCCCATTCCT 16993

RESULT 16
US-09-949-016-12983
; Sequence 12983, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
```

```
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 12983
/ LENGTH: 157866
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-12983
```

```
Query Match          75.0%; Score 15; DB 4; Length 157866;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 TGCACCTCCCATTTCT 19
      |||||
Db      16979 TGCACCTCCCATTTCT 16993
```

```
RESULT 17
US-09-949-016-12984
/ Sequence 12984, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 12984
/ LENGTH: 157866
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-12984
```

```
Query Match          75.0%; Score 15; DB 4; Length 157866;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 TGCACCTCCCATTTCT 19
      |||||
Db      16979 TGCACCTCCCATTTCT 16993
```

```
RESULT 18
US-09-949-016-15779/C
/ Sequence 15779, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
```

```
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 15779
/ LENGTH: 265038
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(265038)
/ OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15779
```

```
Query Match          75.0%; Score 15; DB 4; Length 265038;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 TGCACCTCCCATTTCT 19
      |||||
Db      195654 TGCACCTCCCATTTCT 195640
```

```
RESULT 19
US-09-513-999C-33158
/ Sequence 33158, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Duciart, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ FILE REFERENCE: 59, US2, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO: 33158
/ LENGTH: 272
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-513-999C-33158
```

```
Query Match          70.0%; Score 14; DB 4; Length 272;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 CCACCTCCCATTTCTT 20
      |||||
Db      214 CCACCTCCCATTTCTT 227
```

```
RESULT 20
US-09-949-016-82921
/ Sequence 82921, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 82921
```

LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-82921

Query Match 70.0%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCATTC 18  
|||||  
Db 414 TGGCACTCCCATTC 427

RESULT 21  
US-09-949-016-82922  
Sequence 82922, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C0001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 82922  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-82922

Query Match 70.0%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCATTC 18  
|||||  
Db 396 TGGCACTCCCATTC 409

RESULT 22  
US-09-949-016-132819  
Sequence 132819, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C0001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 132819  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-132819

Query Match 70.0%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCC 14  
|||||  
Db 336 GCATTGCCACTCCC 349

RESULT 23  
US-09-949-016-202121  
Sequence 202121, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C0001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 202121  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-202121

Query Match 70.0%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTCGCATCCCA 15  
|||||  
Db 45 CATTCGCATCCCA 58

RESULT 24  
US-09-540-236-1580/C  
Sequence 1580, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
FILE REFERENCE: 2709,2005-001  
CURRENT APPLICATION NUMBER: US/09/540,236  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 1580  
LENGTH: 618  
TYPE: DNA  
ORGANISM: M.catarhalis  
US-09-540-236-1580

Query Match 70.0%; Score 14; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATCTT 20  
|||||  
Db 399 CCACTCCCATCTT 386

RESULT 25  
US-09-687-698-14/C  
Sequence 14, Application US/09687698

```

; Patent No. 6534067
; GENERAL INFORMATION:
; APPLICANT: Estes, Mary
; TITLE OF INVENTION: A NOVEL ADJUVANT
; FILE REFERENCE: P01883US1
; CURRENT APPLICATION NUMBER: US/09/687,698
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/159,390
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 751
; TYPE: DNA
; ORGANISM: Bovine rotavirus strain B223
; US-09-687-698-14

Query Match
Best Local Similarity 100.0%; DB 4; Length 751;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACTCCCATCTT 20
Db 524 CCACTCCCATCTT 511

RESULT 26
US-09-705-621-30/c
; Sequence 30, Application US/09705621
; Patent No. 667335
; GENERAL INFORMATION:
; APPLICANT: ESTES, MARY
; TITLE OF INVENTION: ROTAVIRUS ENTEROTOXIN NSP4 AND METHODS OF USING SAME
; FILE REFERENCE: P01932US3
; CURRENT APPLICATION NUMBER: US/09/705,621
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 30
; LENGTH: 751
; TYPE: DNA
; ORGANISM: Bovine Rotavirus Strain B223
; US-09-705-621-30

Query Match
Best Local Similarity 100.0%; DB 4; Length 751;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACTCCCATCTT 20
Db 524 CCACTCCCATCTT 511

RESULT 27
US-09-573-080A-424
; Sequence 424, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOOL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 424
; LENGTH: 7417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(7417)
```

```

; OTHER INFORMATION: herVK14cl
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J, Malichiewicz, J, Milosavljevic, A
; TITLE: Protocypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE: 1996-01-26
; DATABASE ENTRY DATE: 1996-01-26
; US-09-573-080A-424

Query Match
Best Local Similarity 100.0%; DB 4; Length 7417;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGCCACTCCCAT 17
Db 712 TTGCCACTCCCAT 725

RESULT 28
US-09-949-016-16540/c
; Sequence 16540, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16540
; LENGTH: 7447
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16540

Query Match
Best Local Similarity 100.0%; DB 4; Length 7447;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGCACTCCCATTC 18
Db 5887 TGGCACTCCCATTC 5874

RESULT 29
US-09-949-016-12313
; Sequence 12313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 12313  
;; LENGTH: 14551  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-12313

Query Match 70.0%; Score 14; DB 4; Length 14551;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACTCCCATCTT 19  
DB 10939 GCCACTCCCATCTT 10952

RESULT 30  
US-09-949-016-16465  
;; Sequence 16465, Application US/09949016  
;; Patent No. 6812339  
;; GENERAL INFORMATION:  
;; APPLICANT: VENTER, J. Craig et al.  
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;; FILE REFERENCE: C0001307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 16465  
;; LENGTH: 14551  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-16465

Query Match 70.0%; Score 14; DB 4; Length 14551;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACTCCCATCTT 19  
DB 10939 GCCACTCCCATCTT 10952

RESULT 31  
US-09-949-016-12826  
;; Sequence 12826, Application US/09949016  
;; Patent No. 6812339  
;; GENERAL INFORMATION:  
;; APPLICANT: VENTER, J. Craig et al.  
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;; FILE REFERENCE: C0001307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 12826

;; LENGTH: 21535  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-12826

Query Match 70.0%; Score 14; DB 4; Length 21535;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATCTT 20  
DB 13459 CCACTCCCATCTT 13472

RESULT 32  
US-09-949-016-12827  
;; Sequence 12827, Application US/09949016  
;; Patent No. 6812339  
;; GENERAL INFORMATION:  
;; APPLICANT: VENTER, J. Craig et al.  
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;; FILE REFERENCE: C0001307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 12827  
;; LENGTH: 21535  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-12827

Query Match 70.0%; Score 14; DB 4; Length 21535;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATCTT 20  
DB 13459 CCACTCCCATCTT 13472

RESULT 33  
US-09-949-016-12828  
;; Sequence 12828, Application US/09949016  
;; Patent No. 6812339  
;; GENERAL INFORMATION:  
;; APPLICANT: VENTER, J. Craig et al.  
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;; FILE REFERENCE: C0001307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 12828  
;; LENGTH: 21535  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-12828

Query Match 70.0%; Score 14; DB 4; Length 21535;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACCTCCCATCTT 20  
|||||  
Db 13459 CCACCTCCCATCTT 13472

RESULT 34  
US-09-949-016-12829  
; Sequence 12829, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12829  
; LENGTH: 21535  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12829

Query Match 70.0%; Score 14; DB 4; Length 21535;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACCTCCCATCTT 20  
|||||  
Db 13459 CCACCTCCCATCTT 13472

RESULT 35  
US-09-949-016-13366  
; Sequence 13366, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13366  
; LENGTH: 21536  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13366

Query Match 70.0%; Score 14; DB 4; Length 21536;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACCTCCCATCTT 20

Db 13459 CCACCTCCCATCTT 13472

RESULT 36  
US-09-949-016-13367  
; Sequence 13367, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13367  
; LENGTH: 21536  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13367

Query Match 70.0%; Score 14; DB 4; Length 21536;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACCTCCCATCTT 20  
|||||  
Db 13459 CCACCTCCCATCTT 13472

RESULT 37  
US-09-949-016-13368  
; Sequence 13368, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13368  
; LENGTH: 21536  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13368

Query Match 70.0%; Score 14; DB 4; Length 21536;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACCTCCCATCTT 20  
|||||  
Db 13459 CCACCTCCCATCTT 13472

RESULT 38

US-09-949-016-13369  
; Sequence 13369, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13369  
; LENGTH: 21536  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13369

Query Match 70.0%; Score 14; DB 4; Length 21536;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATCTT 20  
|||  
Db 13459 CCACTCCCATCTT 13472

RESULT 39  
US-09-596-002-26/c  
; Sequence 26, Application US/09596002  
; Patent No. 6632636  
; GENERAL INFORMATION:  
; APPLICANT: Lagace, Robert, E.  
; APPLICANT: Patterson, Chandra  
; APPLICANT: Berg, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: PM-0008-4 US  
; CURRENT APPLICATION NUMBER: US/09/596,002  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/140,121  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PERL Program  
; SEQ ID NO 26  
; LENGTH: 34279  
; TYPE: DNA  
; ORGANISM: M. catarrhalis  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte template ID No. 6632636 26  
; PUBLICATION INFORMATION:  
US-09-596-002-26

Query Match 70.0%; Score 14; DB 4; Length 34279;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATCTT 20  
|||  
Db 9394 CCACTCCCATCTT 9381

RESULT 40  
US-09-949-016-12149  
; Sequence 12149, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12149  
; LENGTH: 36542  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12149

Query Match 70.0%; Score 14; DB 4; Length 36542;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATCTT 20  
|||  
Db 35042 CCACTCCCATCTT 35055

RESULT 41  
US-09-949-016-13434  
; Sequence 13434, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13434  
; LENGTH: 36544  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13434

Query Match 70.0%; Score 14; DB 4; Length 36544;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATCTT 20  
|||  
Db 35042 CCACTCCCATCTT 35055

RESULT 42  
US-09-949-016-12324/c  
; Sequence 12324, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12324
; LENGTH: 47818
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(47818)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12324
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Query Match          70.0%; Score 14; DB 4; Length 47818;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      5 TGGCACTCCCATTC 18
Db      6301 TGGCACTCCCATTC 6288
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```

RESULT 43
US-09-949-016-15166/c
; Sequence 15166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15166
; LENGTH: 48480
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(48480)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15166
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Query Match          70.0%; Score 14; DB 4; Length 48480;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      5 TGGCACTCCCATTC 18
Db      6301 TGGCACTCCCATTC 6288
```

```

RESULT 44
US-09-949-016-12500/c
; Sequence 12500, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12500
; LENGTH: 53336
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12500
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Query Match          70.0%; Score 14; DB 4; Length 53336;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      6 GCCACTCCCATTCCT 19
Db      21679 GCCACTCCCATTCCT 21666
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RESULT 45
US-09-949-016-16092/c
; Sequence 16092, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16092
; LENGTH: 53337
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16092
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Query Match          70.0%; Score 14; DB 4; Length 53337;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      6 GCCACTCCCATTCCT 19
Db      21679 GCCACTCCCATTCCT 21666
```

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Search completed: August 5, 2005, 02:23:02
Job time : 136 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 10:09:26 ; Search time 427 Seconds  
(without alignments)  
277.271 Million cell updates/sec

Title: US-10-643-801A-35

Perfect score: 20  
Sequence: 1 gcattgcctaccctcttc 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 8

Total number of hits satisfying chosen parameters: 760883

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	469 10 ADD49704	ADD49704 Human lun
2	20	100.0	827 3 AA260383	AA260383 A diacylg
3	20	100.0	885 3 AA260387	AA260387 A diacylg
4	20	100.0	1030 12 AD042678	AD042678 Human NOV
5	20	100.0	1077 12 AD042677	AD042677 Human NOV
6	20	100.0	1167 6 AB153626	AB153626 Breast pr
7	20	100.0	1167 6 AAD46542	AA46542 Mouse dia
8	20	100.0	1167 12 AD015616	AD015616 Mouse DGA
9	20	100.0	1172 12 AD042254	AD042254 Human NOV
10	20	100.0	1189 12 AD042252	AD042252 Human NOV
11	20	100.0	1189 12 AD042258	AD042258 Human NOV
12	20	100.0	1191 12 AD042248	AD042248 Human NOV
13	20	100.0	1191 12 AD042244	AD042244 Human NOV
14	20	100.0	1198 12 AD042256	AD042256 Human NOV
15	20	100.0	1207 12 AD042250	AD042250 Human NOV
16	20	100.0	1230 12 AD042246	AD042246 Human NOV
17	20	100.0	1230 12 AD042679	AD042679 Human NOV
18	20	100.0	1231 6 AAD46541	AA46541 Human dia
19	20	100.0	1231 12 AD015614	AD015614 Human DGA
20	20	100.0	1233 6 AAD46549	AA46549 Human DGA

21	20	100.0	1233 12 AD015631	AD015631 Human acy
22	20	100.0	1303 2 AA233556	AA233556 Human bre
23	20	100.0	1510 13 ADR26804	ADR26804 Breast ca
24	20	100.0	1543 6 AB153628	AB153628 Breast pr
25	20	100.0	1570 3 AA371103	AA371103 Human PRO
26	20	100.0	1570 4 AA54409	AA54409 Primer #8
27	20	100.0	1570 4 AA846092	AA846092 Human DNA
28	20	100.0	1570 8 AAC89542	AA89542 CDNA enco
29	20	100.0	1570 8 ACA73552	ACA73552 Human sec
30	20	100.0	1570 8 ACA05867	ACA05867 Human sec
31	20	100.0	1570 8 ACA66701	ACA66701 CDNA enco
32	20	100.0	1570 8 ACF20276	ACF20276 Human sec
33	20	100.0	1570 8 ACF19662	ACF19662 Human sec
34	20	100.0	1570 8 ACD21950	ACD21950 Human sec
35	20	100.0	1570 8 ACF13115	ACF13115 Human sec
36	20	100.0	1570 8 ACD25218	ACD25218 Human sec
37	20	100.0	1570 8 ACF00267	ACF00267 Human sec
38	20	100.0	1570 8 ACA72324	ACA72324 Novel hum
39	20	100.0	1570 8 ACD04848	ACD04848 Novel hum
40	20	100.0	1570 8 ACD18309	ACD18309 Human sec
41	20	100.0	1570 8 ACD08316	ACD08316 Human sec
42	20	100.0	1570 8 ACA88750	ACA88750 Novel hum
43	20	100.0	1570 8 ACA70192	ACA70192 Human sec
44	20	100.0	1570 8 ACD12414	ACD12414 Novel hum
45	20	100.0	1570 8 ACD74329	ACD74329 Human sec
46	20	100.0	1570 8 ACD15957	ACD15957 Human sec
47	20	100.0	1570 8 ACD25525	ACD25525 Novel hum
48	20	100.0	1570 8 ACD18002	ACD18002 Human sec
49	20	100.0	1570 8 ACC88289	ACC88289 Human sec
50	20	100.0	1570 8 ACD21643	ACD21643 Human sec
51	20	100.0	1570 8 ACD18710	ACD18710 Human sec
52	20	100.0	1570 8 ABX98320	ABX98320 Human cdn
53	20	100.0	1570 8 ACD14071	ACD14071 Human PRO
54	20	100.0	1570 8 ACD09851	ACD09851 Human sec
55	20	100.0	1570 8 ACC88596	ACC88596 Human sec
56	20	100.0	1570 8 ACD21336	ACD21336 Human sec
57	20	100.0	1570 8 ABX75708	ABX75708 Human cdn
58	20	100.0	1570 8 ABX97911	ABX97911 Human PRO
59	20	100.0	1570 8 ACA97387	ACA97387 Novel hum
60	20	100.0	1570 8 ACA57850	ACA57850 Human PRO
61	20	100.0	1570 8 ACD14378	ACD14378 Human PRO
62	20	100.0	1570 8 ACC91161	ACC91161 Human sec
63	20	100.0	1570 8 ACC88903	ACC88903 Human sec
64	20	100.0	1570 8 ACD07100	ACD07100 Human PRO
65	20	100.0	1570 8 ACA67551	ACA67551 Human PRO
66	20	100.0	1570 8 ACC81606	ACC81606 Human sec
67	20	100.0	1570 8 ACC89210	ACC89210 Human sec
68	20	100.0	1570 8 ACC86566	ACC86566 Human sec
69	20	100.0	1570 8 ACC89824	ACC89824 Human sec
70	20	100.0	1570 8 ACC93003	ACC93003 Human sec
71	20	100.0	1570 8 ACA72631	ACA72631 Human PRO
72	20	100.0	1570 8 ACA89149	ACA89149 Human sec
73	20	100.0	1570 8 ACA69885	ACA69885 Human sec
74	20	100.0	1570 8 ACA97028	ACA97028 Novel hum
75	20	100.0	1570 8 ACA91024	ACA91024 Novel hum
76	20	100.0	1570 8 ACA70806	ACA70806 Human sec
77	20	100.0	1570 8 ACA95316	ACA95316 Novel hum
78	20	100.0	1570 8 ACC86259	ACC86259 Human sec
79	20	100.0	1570 8 ACC90131	ACC90131 Human sec
80	20	100.0	1570 8 ACD12739	ACD12739 Human sec
81	20	100.0	1570 8 ACF19969	ACF19969 Human sec
82	20	100.0	1570 8 ABX76913	ABX76913 Human PRO
83	20	100.0	1570 8 ACA73245	ACA73245 Novel hum
84	20	100.0	1570 8 ACA68788	ACA68788 Novel hum
85	20	100.0	1570 8 ACA74632	ACA74632 CDNA enco
86	20	100.0	1570 8 ACA70499	ACA70499 Human sec
87	20	100.0	1570 8 ACD14685	ACD14685 Human PRO
88	20	100.0	1570 8 ACA68357	ACA68357 Novel hum
89	20	100.0	1570 8 ABX98822	ABX98822 Novel hum
90	20	100.0	1570 8 ACC81299	ACC81299 Human sec
91	20	100.0	1570 8 ACA95623	ACA95623 Novel hum
92	20	100.0	1570 8 ACD04541	ACD04541 Novel hum
93	20	100.0	1570 8 ACC87982	ACC87982 Human sec

	94	95	96	97	98	99	100
c	20	100.0	1570	8	ACF12644	Human sec	
c	20	100.0	1570	8	ACA96339	Human PRO	
c	20	100.0	1570	8	ACA65133	Human PRO	
c	20	100.0	1570	8	ACA73859	Human sec	
c	20	100.0	1570	8	ACA74271	Novel hum	
c	20	100.0	1570	8	ACA96666	Human PRO	
c	20	100.0	1570	8	ACD10772	CDNA enco	

## ALIGNMENTS

## RESULT 1

ADD49704/c  
ID ADD49704 standard; cDNA; 469 BP.

ADD49704;

15-JAN-2004 (first entry)

Human lung cancer associated cDNA 61594676.

Human; ss; lung cancer antigen; cyrostatic; lung cancer; gene therapy;

vaccine; T-cell; tumour.

Homo sapiens.

US2003194764-A1.

16-OCT-2003.

04-APR-2002; 2002US-00116712.

05-APR-2001; 2001US-0282289P.

05-OCT-2001; 2001US-0327511P.

(CORI-) CORIXA CORP.

Bangur CS, Switzer A;

WPI; 2003-844452/78.

New isolated polypeptides and polynucleotides useful for diagnosing, preventing and treating cancer, particularly lung cancer.

Claim 1, SEQ ID NO 436; 250bp; English.

The invention relates to an isolated polynucleotide (a) comprising any of the 666 fully defined nucleotide sequences appearing as ADD49269 - ADD49935, ADD49936 and ADD49938, complements of (a); sequences of at least 20 contiguous residues of (a); sequences that hybridise to (a) under highly stringent conditions; sequences having at least 75 or 90% identity to (a); or degenerate variants of (a). Also included are an isolated polypeptide (b) (comprising: sequences encoded by the new polynucleotide; any of the 4 amino acid sequences fully defined in the specification; or sequences having at least 70 or 90% identity to the sequence in (a) or (b)), an expression vector comprising the above polynucleotide operably linked to an expression control sequence, a host cell transformed or transfected with the above expression vector, an isolated antibody, or its antigen-binding fragment, that specifically binds to the above polypeptide, an oligonucleotide that hybridises to the above-mentioned nucleotide sequences under highly stringent conditions, a fusion protein comprising at least one polypeptide cited above, detecting the presence of a cancer in a patient (comprising: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide, or with the oligonucleotide cited above; detecting in the sample an amount of the polypeptide that binds to the binding agent, or an amount of a polynucleotide that hybridises to the oligonucleotide; and comparing the amount of polypeptide, or polynucleotide that hybridises to the oligonucleotide, to a predetermined cut-off value and then determining the presence of a cancer in the patient), a method for stimulating and/or expanding T-cells specific for a tumour protein (comprising contacting T-cells with the above

polypeptide, polynucleotide or antigen-presenting cells that express the polynucleotide, under conditions and for a time sufficient to permit the stimulation and/or expansion of T-cells), an isolated T-cell population comprising T-cells prepared by the method, a composition comprising a first component selected from physiological carriers and second component selected from physiological carriers and a second component selected from the above polypeptide, polynucleotide, antibody, fusion protein, T-cell population and antigen-presenting cells that express the above polypeptide, stimulating an immune response in a patient (comprising administering to the patient the above composition) treating lung cancer in a patient (comprising administering to the patient the above composition and a diagnostic kit (comprising: at least one oligonucleotide cited above; or at least one antibody cited above and a detection reagent, where the detection reagent comprises a reporter group). The composition and methods are useful in diagnosing, preventing and treating cancer, particularly lung cancer. The present sequence is a lung cancer-associated antigen cDNA of the invention.

Sequence 469 BP; 105 A; 123 C; 136 G; 105 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 469;

Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Indels 0;

1 GCATTGCCACTCCATTCTT 20

269 GCATTGCCACTCCATTCTT 250

## RESULT 2

AAZ60383/c

AAZ60383 standard; DNA; 827 BP.

AAZ60383;

05-MAY-2000 (first entry)

A diacylglycerol acyl transferase related expressed sequence tag.

Diacylglycerol acyl transferase; DAGAT; triacylglycerol; diacylglycerol;

fatty acyl substrate; lipid composition; plant cell; fatty acid;

plant seed oil; chylomicra; small intestine;

very low density lipoprotein; liver; energy storage; adipose tissue;

lipid absorption; plasma triglyceride level; adipogenesis;

protein kinase C; cancer; diabetes; cardiopulmonary disease;

atherosclerosis; adipocytosis; leukaemia; fibroblastoma;

metabolic disorder; obesity; lipid metabolism; fat absorption;

expressed sequence tag; Mortierella ramanniana; ss.

Homo sapiens.

WO200001713-A2.

13-JAN-2000.

30-JUN-1999; 99WO-US015243.

02-JUL-1998; 98US-0091631P.

23-APR-1999; 99US-0130829P.

(CALJ) CALGENE LLC.

Lardizabal KD, Hawkins D, Thompson GA;

WPI; 2000-170997/15.

New Mortierella ramanniana DNA encoding diacylglyceroltransferase for producing transgenic plants or for treating the enzyme associated diseases.

Claim 9; Page 104; 114pp; English.

The present sequence represents a contig of expressed sequence tags

(ESTs) which are related to the Mortierella ramanniana diacylglycerol acyl transferase (DAGAT) sequence. The DAGAT enzyme is active in the formation of triacylglycerol from diacylglycerol and fatty acyl substrates. The DNA sequences encoding DAGAT can be used to modify the triacylglycerol and lipid composition of plant cells. The DAGAT DNA sequences may be in sense or antisense orientations to enhance or suppress activity of endogenous DAGAT. DAGAT constructs are useful for genetically altering plants to produce a particular fatty acid in the plant seed oil. Antagonists and agonists of DAGAT activity are useful as DAGAT is important in the formation of chylomicra in small intestine, very low density lipoprotein in liver and for storage of energy as triacylglycerol in adipose tissue. Thus, inhibiting DAGAT activity in small intestine, liver and adipose tissue will reduce lipid absorption and plasma triglyceride levels and will decrease adipogenesis. Agonists and antagonists are particularly useful in treating diseases associated with altered cellular diacylglycerol concentration or protein kinase C activity, including cancer, diabetes, cardiopulmonary diseases, atherosclerosis, adipocytosis, leukaemia, fibroblastoma, metabolic disorders, obesity and diseases associated with abnormal lipid metabolism and fat absorption

Sequence 827 BP; 174 A; 230 C; 227 G; 196 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 827;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCATCCCATCTT 20  
|||  
Db 479 GCATTGCCATCCCATCTT 460

#### RESULT 3

AA260387/c  
ID AA260387 standard; DNA; 885 BP.

AA260387;

05-MAY-2000 (first entry)

A diacylglycerol acyl transferase related expressed sequence tag.

Diacylglycerol acyl transferase; DAGAT; triacylglycerol; diacylglycerol; fatty acyl substrate; lipid composition; plant cell; fatty acid; plant seed oil; chylomicra; small intestine; very low density lipoprotein; liver; energy storage; adipose tissue; lipid absorption; plasma triglyceride level; adipogenesis; protein kinase C; cancer; diabetes; cardiopulmonary disease; atherosclerosis; adipocytosis; leukaemia; fibroblastoma; metabolic disorder; obesity; lipid metabolism; fat absorption; expressed sequence tag; Mortierella ramanniana; ss.

Mus sp.

WO200001713-A2.

13-JAN-2000.

30-JUN-1999; 99WO-US015243.

02-JUL-1998; 98US-0091631P.

23-APR-1999; 99US-0130829P.

(CALJ) CALGENE LLC.

Lardizabal KD, Hawkins D, Thompson GA;

WPI. 2000-170997/15.

New Mortierella ramanniana DNA encoding diacylglyceroltransferase for producing transgenic plants or for treating the enzyme associated diseases.

PS Claim 9; Page 105; 114pp; English.

The present sequence represents a contig of expressed sequence tags (ESTs) which are related to the Mortierella ramanniana diacylglycerol acyl transferase (DAGAT) sequence. The DAGAT enzyme is active in the formation of triacylglycerol from diacylglycerol and fatty acyl substrates. The DNA sequences encoding DAGAT can be used to modify the triacylglycerol and lipid composition of plant cells. The DAGAT DNA sequences may be in sense or antisense orientations to enhance or suppress activity of endogenous DAGAT. DAGAT constructs are useful for genetically altering plants to produce a particular fatty acid in the plant seed oil. Antagonists and agonists of DAGAT activity are useful as DAGAT is important in the formation of chylomicra in small intestine, very low density lipoprotein in liver and for storage of energy as triacylglycerol in adipose tissue. Thus, inhibiting DAGAT activity in small intestine, liver and adipose tissue will reduce lipid absorption and plasma triglyceride levels and will decrease adipogenesis. Agonists and antagonists are particularly useful in treating diseases associated with altered cellular diacylglycerol concentration or protein kinase C activity, including cancer, diabetes, cardiopulmonary diseases, atherosclerosis, adipocytosis, leukaemia, fibroblastoma, metabolic disorders, obesity and diseases associated with abnormal lipid metabolism and fat absorption

Sequence 885 BP; 190 A; 246 C; 240 G; 204 T; 0 U; 5 Other;

Query Match 100.0%; Score 20; DB 3; Length 885;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCATCCCATCTT 20  
|||  
Db 482 GCATTGCCATCCCATCTT 463

#### RESULT 4

ADO42678  
ID ADO42678 standard; cDNA; 1030 BP.

ADO42678;

15-JUL-2004 (first entry)

Human NOVX-related polynucleotide #9.

Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes; Alzheimer's disease; Parkinson's disease; graft-versus-host disease; scleroderma; hypertension; haemophilia; idiopathic thrombocytopenic purpura; immunodeficiency; AIDS; dyliipidemia; obesity; Crohn's disease; bronchial asthma; anorexia; cancer-associated cachexia; multiple sclerosis; fertility.

Homo sapiens.

US2004058338-A1.

25-MAR-2004.

02-DEC-2002; 2002US-00307817.

03-DEC-2001; 2001US-0336881P.

05-DEC-2001; 2001US-0336820P.

07-DEC-2001; 2001US-0338285P.

07-DEC-2001; 2001US-0338318P.

10-DEC-2001; 2001US-0338989P.

10-DEC-2001; 2001US-0339022P.

11-DEC-2001; 2001US-0339314P.

11-DEC-2001; 2001US-0339516P.

11-DEC-2001; 2001US-0339517P.

11-DEC-2001; 2001US-0339611P.

12-DEC-2001; 2001US-0340981P.

12-DEC-2001; 2001US-0341346P.

14-DEC-2001; 2001US-0340390P.

PA	(PART//)	PATURAJAN M.
PA	(PEN//)	PENA C E A.
PA	(PEYM//)	PEYMAN J A.
PA	(RIEG//)	RIEGER D K.
PA	(ROTH//)	ROTHENBERG M E.
PA	(SHEN//)	SHENOV S G.
PA	(SMT//)	SMITHSON G.
PA	(SPAD//)	SPADERNA S K.
PA	(SPT//)	SPETER K A.
PA	(STON//)	STONE D J.
PA	(TAUP//)	TAUPIER R J.
PA	(VERN//)	VERNET C A M.
PA	(VOSS//)	VOSS E Z.
PA	(ZHON//)	ZHONG M.
XX		
PI	Agree ML,	Alsbrook JP, Anderson DW, Berghs C, Boldog FL;
PI	Burgess CE,	Catterton E, Dipippo VA, Edinger SK, Eisen A;
PI	Ellerman K,	Ganigoll BA, Gerlach V, Gorman L, Roehberg BG, Guo XS;
PI	Herrman JL,	Haltvorsen Y, Ji W, Kekuda R, Khramtsov NV;
PI	Iarochalle WJ,	Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;
PI	Padiganu M,	Patturajan M, Pena CE, Peyman JA, Rieger DK;
PI	Robdenberg ME,	Sheroy SG, Smitson G, Spaderna SK, Sytek KA;
PI	Stone DJ,	Taupier RJ, Vernet CM, Voss EZ, Zhong M;
XX		
DR	WPI, 2004-268786/25.	
PT	New human NOVX polypeptides and nucleic acid molecules, useful for	
PT	diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,	
PT	atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or	
PT	scleroderma.	
XX		
PS	Example F; SEQ ID NO 539; 610bp; English.	
XX		
CC	The invention relates to human NOVX polypeptides and the polynucleotides	
CC	encoding them. The invention also relates to antibodies specific to the	
CC	NOVX polypeptides. The polypeptides, polynucleotides and antibodies are	
CC	useful for manufacturing a medicament for treating a syndrome associated	
CC	with a human disease, such as a pathology associated with the NOVX	
CC	polypeptide. The sequences are useful for diagnosing, treating or	
CC	preventing a NOVX-associated disorder, e.g. cancer, atherosclerosis,	
CC	diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host	
CC	disease, scleroderma, hypertension, haemophilia, idiopathic	
CC	chromocytogenic purpura, immunodeficiencies, AIDS, dyslipidemia,	
CC	obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated	
CC	cachexia, multiple sclerosis or fertility. The nucleic acids may be used	
CC	as hybridisation probes, in chromosome mapping, in tissue typing, in	
CC	preventive medicine or in pharmacogenomics. This sequence represents a	
CC	human NOVX-related polynucleotide of the invention.	
XX		
SEQ	Sequence 1030 BP; 235 A; 292 C; 286 G; 217 T; 0 U; 0 Other;	
Query Match	100.0%; Score 20; DB 12; Length 1030;	
Best Local Similarity	100.0%; Pred. No. 0.1;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GCATTGCCATCTCCATTCCTT 20	
DB	274 GCATTGCCATCTCCATTCCTT 293	
RESULT 5		
ADO42677		
ID	ADO42677 standard; cDNA; 1077 BP.	
XX		
XX	ADO42677;	
XX		
DT	15-JUN-2004 (first entry)	
XX		
DE	Human NOVX-related polynucleotide #8.	
XX		
XX	Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;	
XX	Alzheimer's disease; Parkinson's disease; graft-versus-host disease;	
XX	scleroderma; hypertension; haemophilia;	

KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;  
 KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;  
 KW cancer-associated cachexia; multiple sclerosis; fertility.  
 OS Homo sapiens.  
 PN US2004058338-A1.  
 PD 25-MAR-2004.  
 XX 02-DEC-2002; 2002US-00307817.  
 XX 03-DEC-2001; 2001US-0336881P.  
 PR 05-DEC-2001; 2001US-0336820P.  
 PR 07-DEC-2001; 2001US-0338285P.  
 PR 10-DEC-2001; 2001US-0338318P.  
 PR 10-DEC-2001; 2001US-0338989P.  
 PR 11-DEC-2001; 2001US-0339022P.  
 PR 11-DEC-2001; 2001US-0339314P.  
 PR 11-DEC-2001; 2001US-0339516P.  
 PR 11-DEC-2001; 2001US-0339517P.  
 PR 12-DEC-2001; 2001US-0339611P.  
 PR 12-DEC-2001; 2001US-0340981P.  
 PR 14-DEC-2001; 2001US-0341346P.  
 PR 14-DEC-2001; 2001US-0340390P.  
 PR 14-DEC-2001; 2001US-0340440P.  
 PR 14-DEC-2001; 2001US-0340565P.  
 PR 14-DEC-2001; 2001US-0340608P.  
 PR 14-DEC-2001; 2001US-0341144P.  
 PR 17-DEC-2001; 2001US-0341477P.  
 PR 17-DEC-2001; 2001US-0341540P.  
 PR 18-DEC-2001; 2001US-0341768P.  
 PR 20-DEC-2001; 2001US-0342592P.  
 PR 31-DEC-2001; 2001US-0344903P.  
 PR 01-FEB-2002; 2002US-0353286P.  
 PR 01-FEB-2002; 2002US-0353288P.  
 PR 26-FEB-2002; 2002US-0359599P.  
 PR 26-FEB-2002; 2002US-0359626P.  
 PR 26-FEB-2002; 2002US-0359671P.  
 PR 27-FEB-2002; 2002US-0359914P.  
 PR 27-FEB-2002; 2002US-0359956P.  
 PR 28-FEB-2002; 2002US-0360924P.  
 PR 28-FEB-2002; 2002US-0360964P.  
 PR 28-FEB-2002; 2002US-0361028P.  
 PR 28-FEB-2002; 2002US-0361255P.  
 PR 28-FEB-2002; 2002US-0361264P.  
 PR 05-MAR-2002; 2002US-0361770P.  
 PR 05-MAR-2002; 2002US-0362230P.  
 PR 13-MAR-2002; 2002US-0364181P.  
 PR 13-MAR-2002; 2002US-0364238P.  
 PR 15-MAR-2002; 2002US-0364978P.  
 PR 15-MAR-2002; 2002US-0365025P.  
 PR 17-APR-2002; 2002US-0373288P.  
 PR 15-MAY-2002; 2002US-0380981P.  
 PR 16-MAY-2002; 2002US-0381004P.  
 PR 17-MAY-2002; 2002US-0381495P.  
 PR 28-MAY-2002; 2002US-0383534P.  
 PR 28-MAY-2002; 2002US-0383744P.  
 PR 29-MAY-2002; 2002US-0383829P.  
 PR 29-MAY-2002; 2002US-0384024P.  
 PR 02-JUL-2002; 2002US-0393338P.  
 PR 06-AUG-2002; 2002US-0401315P.  
 PR 07-AUG-2002; 2002US-0401788P.  
 PR 20-AUG-2002; 2002US-0404767P.  
 PR 23-AUG-2002; 2002US-0405400P.  
 PR 23-AUG-2002; 2002US-0405684P.  
 PR 23-AUG-2002; 2002US-0405687P.  
 PR 23-AUG-2002; 2002US-0405698P.  
 PR 26-AUG-2002; 2002US-0406353P.  
 XX (AGEE/) AGE E M L.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (ANDE/) ANDERSON D W.

PA (BERG/) BERGS C.  
 PA (BOLD/) BOLDG F L.  
 PA (BURG/) BURGESS C E.  
 PA (CAT/) CATTERTON E.  
 PA (DIP/) DIPIPPO V A.  
 PA (EDIN/) EDINGER S R.  
 PA (EISE/) EISEN A.  
 PA (ELLE/) ELLERMAN K.  
 PA (GANG/) GANGOLLI E A.  
 PA (GERL/) GERLACH V.  
 PA (GORM/) GORMAN L.  
 PA (ROTH/) ROTHBERG B G.  
 PA (GUOX/) GUO X S.  
 PA (HERR/) HERRMANN J L.  
 PA (HALV/) HALVORSEN Y.  
 PA (JTW/) JI W.  
 PA (KERU/) KEKUDA R.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (LARO/) LAROCHELLE W J.  
 PA (LEPL/) LEFLEY D M.  
 PA (LILL/) LI L.  
 PA (MACD/) MACDOUGALL J R.  
 PA (MILL/) MILLER C E.  
 PA (ORT/) ORT T.  
 PA (PADI/) PADIGARU M.  
 PA (PAT/) PATTURAJAN M.  
 PA (PENNA/) PENNA C E A.  
 PA (PEYM/) PEYMAN J A.  
 PA (RIEG/) RIEGER D K.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (SHEN/) SHENOY S G.  
 PA (SMIT/) SMITHSON G.  
 PA (SPAD/) SPADERNA S K.  
 PA (SPYT/) SPYTEK K A.  
 PA (STON/) STONE D J.  
 PA (TAUP/) TAUPIER R J.  
 PA (VERN/) VERNET C A M.  
 PA (VOSS/) VOSS E Z.  
 PA (ZHON/) ZHONG M.  
 XX Agge WL, Alsobrook JP, Anderson DM, Berghs C, Boldog FL;  
 PI Bugees CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;  
 PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;  
 PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV;  
 PI Larochelel WJ, Lefley DM, Li L, MacDougall JR, Miller CE, Ort T;  
 PI Padigaru M, Paturajan M, Penna CE, Peyman JA, Rieger DK;  
 PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;  
 PI Stone DJ, Taupier RJ, Vernet CM, Voss EZ, Zhong M;  
 XX WPI: 2004-268786/25.  
 DR  
 XX  
 PT New human NOXV polypeptides and nucleic acid molecules, useful for  
 PT diagnosing, preventing or treating NOXV-associated disorder, e.g. cancer,  
 PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or  
 PT scleroderma.  
 PT  
 XX  
 PS Example E; SEQ ID NO 538; 610pp; English.  
 XX  
 CC The invention relates to human NOXV polypeptides and the polynucleotides  
 CC encoding them. The invention also relates to antibodies specific to the  
 CC NOXV polypeptides. The polypeptides, polynucleotides and antibodies are  
 CC useful for manufacturing a medicament for treating a syndrome associated  
 CC with a human disease, such as a pathology associated with the NOXV  
 CC polypeptide. The sequences are useful for diagnosing, treating or  
 CC preventing a NOXV-associated disorder, e.g., cancer, atherosclerosis,  
 CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host  
 CC disease, scleroderma, hypertension, haemophilia, idiopathic  
 CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,  
 CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated  
 CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used  
 CC as hybridisation probes, in chromosome mapping, in tissue typing, in  
 CC preventive medicine or in pharmacogenomics. This sequence represents a  
 CC human NOXV-related polynucleotide of the invention.

XX	Sequence	1077 BP; 238 A; 295 C; 311 G; 223 T; 0 U; 0 Other;
XX	Query Match	100.0%; Score 20; DB 12; Length 1077;
XX	Best Local Similarity	100.0%; Pred.No. 0.1;
XX	Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 GCATTGCCACTCCCATTCCTT	20
DB		
DB	384 GCATTGCCACTCCCATTCCTT	403
RESULT 6	ABLS53626/c	
ID	ABLS53626	standard; cDNA; 1167 BP.
XX	ABLS53626;	
AC	17-JUN-2002	(first entry)
XX	17-JUN-2002	
DE	Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1)	cDNA.
XX	BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;	
KM	cytostatic; differential expression; gene; ss.	
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FH	CDS	1..1167
FT		/*tag= a
FT		/product= "BSTP-ECG1"
XX	W0200208260-A2.	
PN	31-JAN-2002.	
PD	26-JUL-2001; 2001MO-US023439.	
XX	26-JUL-2001; 2000US-0220967P.	
XX	26-JUL-2000; 2000US-0220967P.	
PR	06-DEC-2000; 2000US-0251669P.	
XX	(STRD ) UNIV STANFORD.	
PA	(GENO-) APPLIED GENOMICS INC.	
XX	Botstein D, Brown PO, Perou C, Ross D, Seltz R;	
PI	WPI; 2002-315251/35.	
XX	P-PSDB; ABB75677.	
DR		
XX		
PT	Novel substantially purified polypeptide encoded by breast protein-	
FT	eukaryotic conserved gene 1, useful for diagnosing, treating or	
PT	preventing breast cancer, and for classifying cancer.	
XX	Claim 2; Fig 1B; 127p; English.	
XX	The present sequence is that of the coding region of BSTP-ECG1 (breast	
XX	protein-eukaryotic conserved gene 1) cDNA, which encodes a 388-amino acid	
CC	protein (see ABB73677). In order to identify genes that are	
CC	differentially expressed in breast tumours, cDNA microarrays were	
CC	produced, each representing the same set of approximately 8100 different	
CC	human genes. Variations in patterns of gene expression were characterised	
CC	in 62 breast tumour samples from 40 patients, 3 normal breast tissue	
CC	samples and 19 samples from 17 human cell lines. IMAGE clone 161484 was	
CC	identified based on the expression pattern of its mRNA among these 84	
CC	samples. Overlapping clones (IMAGE clones 48805, 1276329, 1343900 and	
CC	1560966) were identified in a database search, and a consensus sequence	
CC	(see ABL53629) was produced, from which the present coding region is	
CC	derived. BSTP-ECG1 is differentially expressed among breast tumours. The	
CC	discovery of BSTP-ECG1 and its differential expression are useful for the	
CC	diagnosis, treatment and prevention of cancer, especially breast cancer,	
CC	and provides methods useful in tumour classification and prognosis. BSTP-	
CC	ECG1 is probably a transmembrane protein, making it accessible to	
CC	therapeutic agents such as antibodies and/or small molecules. The gene	

CC	may also be a useful target for therapeutic intervention. The invention provides BSRP-ECG1 polypeptides and polynucleotides, expression vectors,
CC	host cells, antibodies, agonists and antagonists. It also provides methods for treating or preventing disorders of cell proliferation,
CC	particularly breast cancer, by administering a polypeptide, polynucleotide or antibody of the invention. Also provided are methods of classifying diseases, particularly breast cancer by detecting expression of BSRP-ECG1 or a polynucleotide encoding it, and of providing CC diagnostic, prognostic and/or predictive information for patients based CC on the detection and/or measurement of BSRP-ECG1 or polynucleotide CC encoding BSRP-ECG1
SQ	Sequence 1167 BP; 247 A; 338 C; 327 G; 255 T; 0 U; 0 Other;
Query Match	100.0%; Score 20; DB 6; Length 1167;
Best Local Similarity	100.0%; Pred. No. 0.1;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GCATTGCCACATCCCATTTCTT 20         Db 698 GCATTGCCACATCCCATTTCTT 679
RESULT 7	AAD46542/C
ID	AAD46542 standard; cDNA; 1167 BP.
XX	AAD46542;
AC	
XX	27-JAN-2003 (first entry)
DT	
XX	
DE	Mouse diacylglycerol acyltransferase (DGAT) 2alpha cDNA.
XX	
KW	Mouse; monoacylglycerol acyltransferase; MGAT; hypertri-glycaemia; DGAT; diacylglycerol acyltransferase; obesity; anorectic; hypoglycaemic; KM enzyme; gene; ds. XX
OS	Mus musculus.
XX	
FH	Location/Qualifiers
CDS	1..1167
FT	/tag=
FT	/product= "Mouse DGAT2alpha protein"
FT	/transl_except=(pos:58..60, aa:Lys)
FT	/transl_except=(pos:61..63, aa:Pro)
FT	/transl_except=(pos:64..66, aa:Ala)
FT	/transl_except=(pos:67..69, aa:Lys)
FT	/transl_except=(pos:70..72, aa:Lys)
FT	/transl_except=(pos:643..645, aa:Lys)
FT	/transl_except=(pos:895..903, aa:Val-Lys)
PN	WO200268595-A2.
XX	
PD	06-SEP-2002.
XX	
PE	21-FEB-2002; 2002MO-US005474.
XX	
PR	23-FEB-2001; 2001US-0271307P.
PR	26-FEB-2001; 2001US-0079471S.
PR	14-JAN-2002; 2002US-00046924.
PA	(REGC ) UNIV CALIFORNIA.
FI	Cases S, Stone S, Zhou P, Farese RV, Yen CB;
DR	WPJ; 2002-723199/78.
DR	P-PSDB; AAE29027.
XX	New mammalian polynucleotide encoding a polypeptide that exhibits monocacylglycerol and/or diacylglycerol transferase activity, useful for treating a disease condition e.g. hypertri-glycemia or obesity. Claim 1; Fig 6B; 85BP; English.

XX The invention relates to a mammalian polynucleotide present in other than  
 CC its natural environment and encodes a polypeptide that exhibits  
 CC monoacylglycerol (MGAT; E.C. 2.3.1.22) and/or diacylglycerol  
 CC acyltransferase activity (DGAT; E.C. 2.3.1.20). The composition  
 CC comprising the DGAT2alpha or MGAT1 polynucleotide or polypeptide is  
 CC useful for treating a disease condition e.g. hypertriglyceridaemia or  
 CC obesity. The present sequence is mouse DGAT2alpha cDNA  
 XX

SO Sequence 1167 BP; 258 A; 330 C; 320 G; 256 T; 0 U; 3 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 1167;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCATCCCATCTT 20  
 |||||  
 Db 698 GCATTGCCATCCCATCTT 679

RESULT 8  
 ADO15616/c  
 ID ADO15616 standard; cDNA; 1167 BP.  
 AC  
 AC ADO15616;  
 XX  
 XX 12-AUG-2004 (first entry)  
 DE Mouse DGAT2alpha encoding cDNA SEQ ID NO:3.  
 XX  
 XX monoacylglycerol acyltransferase; MGAT; EC 2.3.1.22;  
 KW diacylglycerol transferase; DGAT; EC 2.3.1.20; enzyme; cardiovascular;  
 KW anorectic; antilipemic; antidiabetic; cytostatic; neuroprotective;  
 KW diacylglyceride; triglyceride; acylglycerol metabolism;  
 KW cardiovascular disease; hyperlipidaemia; obesity; diabetes; cancer;  
 KW neurological disorder; immunological disorder; gene therapy; mouse;  
 KW diacylglycerol O-acyltransferase 2 alpha; DGAT2alpha; gene; ss.  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT 1..1167  
 FT CDS  
 FT /\*tag= a  
 FT /product= "DGAT2alpha"  
 FT /transl\_except= (pos:58..72,aa:LPPAK)  
 FT /transl\_except= (pos:663..665,aa:Leu)  
 FT /transl\_except= (pos:898..903,aa:Iys)  
 XX  
 XX MO2004042014-A2.  
 XX  
 XX 21-MAY-2004.  
 XX  
 XX 29-OCT-2003; 2003WO-US034598.  
 XX  
 XX 31-OCT-2002; 2002US-00286581.  
 XX  
 XX (GLAD-) GLADSTONE INST J DAVID.  
 PA  
 PI Cases S, Stone SJ, Zhou P, Farese RV, Yen CE;  
 XX  
 XX WPI; 2004-400668/37.  
 DR P-PsDB; ADO15617.  
 DR  
 XX  
 XX New mammalian monoacylglycerol acyltransferase 2 polypeptide, useful for  
 FT treating cardiovascular disease, hyperlipidemia, obesity, diabetes,  
 PT cancer, neurological disorders and immunological disorders.  
 XX  
 XX Example 1; SEQ ID NO 3; 98bp; English.  
 PS  
 XX The present invention describes a mammalian monoacylglycerol  
 CC acyltransferase (MGAT, EC 2.3.1.22) polypeptide (1a) and a diacylglycerol  
 CC transferase (DGAT, EC 2.3.1.20) polypeptide (1b) present in other than  
 CC its naturally occurring environment. Also described: (1) a mammalian

CC polynucleotide (1i) present in other than its natural environment  
 CC encoding a polypeptide that exhibits MGAT and/or DGAT activity; (2) an  
 CC expression cassette (1ii) comprising a transcriptional initiation region  
 CC functional in an expression host; (1i) under the transcriptional  
 CC regulation of the transcriptional initiation region, and transcriptional  
 CC comprising (1ii) as a part of an extrachromosomal element or integrated  
 CC into the genome of a host cell as a result of introducing (1i) into the  
 CC host cell; (4) cellular progeny (V) of (1v); (5) preparing (1a) and/or  
 CC (1b); (6) monoclonal antibody (VI) binding specifically to (1a) or (1b);  
 CC (7) inhibiting (MI) the activity of (1a) or (1b); and (8) identifying an  
 CC agent that inhibits an acyltransferase activity of MGAT2 polypeptide.  
 CC (1a) and (1b) have cardiovascular, anorectic, antilipemic, antidiabetic,  
 CC cyostatic and neuroprotective activities. (1a) can be used for producing  
 CC in vitro models of diglyceride and/or triglyceride synthesis, and for  
 CC producing triglyceride compositions which find use in foodstuffs,  
 CC spreads, cooking materials, feedstocks and in industries for producing  
 CC chemicals, lubricants and surfactants. (1a), (1b) and (VI) are useful for  
 CC treating disease conditions associated with acylglycerol metabolism,  
 CC particularly associated with diacylglycerol O-acyltransferase 2 alpha  
 CC (DGAT2alpha). MGAT1 or MGAT2 activity. The disease conditions include  
 CC cardiovascular disease, hyperlipidaemia, obesity, diabetes, cancer,  
 CC neurological disorders and immunological disorders. (1ii) can be in gene  
 CC therapy to treat disorders associated with DGAT2alpha, MGAT1 or MGAT2  
 CC defects, as probes and primers in hybridisation applications (e.g., PCR),  
 CC for identifying expression patterns in biological specimens, for  
 CC preparing cell or animal models for DGAT2alpha, MGAT1 or MGAT2 function,  
 CC for preparing in vitro models for (DGAT2alpha), MGAT1 or MGAT2 function,  
 CC to generate transgenic host. The present sequence encodes mouse  
 CC DGAT2alpha, which is used in the exemplification of the present  
 CC invention.  
 XX

SO Sequence 1167 BP; 258 A; 330 C; 320 G; 256 T; 0 U; 3 Other;  
 Query Match 100.0%; Score 20; DB 12; Length 1167;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCATCCCATCTT 20  
 |||||  
 Db 698 GCATTGCCATCCCATCTT 679

RESULT 9  
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 AC  
 AC ADO42254;  
 XX  
 XX 15-JUN-2004 (first entry)  
 DE Human NOVA polynucleotide #52.  
 XX  
 XX Human; NOVA; gene; ss; cancer; atherosclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;  
 KW scleroderma; hypertension; haemophilia;  
 KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;  
 KW dyslipidaemia; obesity; Crohn's disease; bronchial asthma; anorexia;  
 KW cancer-associated cachexia; multiple sclerosis; fertility.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX US2004058338-A1.  
 PN  
 XX  
 XX 25-MAR-2004.  
 PD  
 XX  
 XX 02-DEC-2002; 2002US-00307817.  
 PF  
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 XX 03-DEC-2001; 2001US-0336881P.  
 PR 05-DEC-2001; 2001US-0336820P.  
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 PR 10-DEC-2001; 2001US-0338318P.  
 PR 10-DEC-2001; 2001US-0338989P.

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PR 10-DEC-2001; 2001US-0339022P.
PR 11-DEC-2001; 2001US-0339314P.
PR 11-DEC-2001; 2001US-0339516P.
PR 11-DEC-2001; 2001US-0339517P.
PR 11-DEC-2001; 2001US-0339611P.
PR 12-DEC-2001; 2001US-0340981P.
PR 12-DEC-2001; 2001US-0341346P.
PR 14-DEC-2001; 2001US-0340390P.
PR 14-DEC-2001; 2001US-0340440P.
PR 14-DEC-2001; 2001US-0340565P.
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PR 17-DEC-2001; 2001US-0341477P.
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PR 20-DEC-2001; 2001US-0342592P.
PR 31-DEC-2001; 2001US-03444903P.
PR 01-FEB-2002; 2002US-0353286P.
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PR 13-MAR-2002; 2002US-0364181P.
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PR 15-MAR-2002; 2002US-0364978P.
PR 15-MAR-2002; 2002US-0376025P.
PR 17-APR-2002; 2002US-0373288P.
PR 15-MAY-2002; 2002US-0380981P.
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PR 02-JUL-2002; 2002US-0393332P.
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XX
XX (AGRE/) AGEE M. L.
PA (ALSO/) AGESBROOK J. P.
PA (ANDE/) ANDERSON D. W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F. L.
PA (BURG/) BURGESS C. E.
PA (CATT/) CATTERTON E.
PA (DIRI/) DIPIPPO V. A.
PA (EDIN/) EDINGER S. R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E. A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTBERG B. G.
PA (GUOX/) GUO X. S.
PA (HERR/) HERRMANN J. L.
PA (HALV/) HALVORSEN Y.
PA (JIWV/) JI W.
PA (KEKU/) KEKUDA R.
PR 10-DEC-2001; 2001US-0339022P.
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PR 05-MAR-2002; 2002US-0361770P.
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PR 13-MAR-2002; 2002US-0364181P.
PR 13-MAR-2002; 2002US-0364238P.
PR 15-MAR-2002; 2002US-0364978P.
PR 15-MAR-2002; 2002US-0376025P.
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XX
XX (KIRA/) KIRAMTSOV N. V.
PA (LARO/) LAROCHELLE W. J.
PA (LEPL/) LEPLLEY D. M.
PA (LITL/) LI L.
PA (MACD/) MACDOUGALL J. R.
PA (MILL/) MILLER C. E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C. E. A.
PA (PEYM/) PEYMAN J. A.
PA (RIEG/) RIEGER D. K.
PA (ROTH/) ROTHEBERG M. E.
PA (SHEN/) SHENOY S. G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S. K.
PA (SPYT/) SPYTEK K. A.
PA (STON/) STONE D. J.
PA (TAUP/) TAUPIER R. J.
PA (VERN/) VERNET C. A. M.
PA (VOSS/) VOSS B. Z.
PA (ZHON/) ZHONG M.
XX
XX Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL,
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A,
PI Ellerman K, Gangolli BA, Gerlach V, Gorman L, Rothberg BG, Guo XS,
PI Herrman JL, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV,
PI Iarochalle WJ, Lepley DM, Li L, MacDougall JR, Miller CE, Ort T,
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Rieger DK, Ort T,
PI Rotenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA,
PI Stone DJ, Taupier RJ, Vernet CM, Voss EZ, Zhong M;
XX
XX MPI; 2004-268786/25.
DR P-PSDB; ADO42255.
XX
XX New human NOXV polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOXV-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
XX Claim 20; SEQ ID NO 103; 610pp; English.
XX
XX The invention relates to human NOXV polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOXV polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOXV
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOXV-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOXV polynucleotide of the invention.
XX
XX
XX Sequence 1172 BP; 248 A; 343 C; 327 G; 254 T; 0 U; 0 Other;
SQ

```

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Query Match 100.0%; Score 20; DB 12; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCATTGCACTCCCATCTT 20
DB 703 GCATTGCACTCCCATCTT 684

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RESULT 10
ADO42252/c
ID ADO42252 standard; CDNA; 1189 BP.
XX

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AC ADO42252;
XX
XX 15-JUL-2004 (first entry)
XX
DE Human NOVX polynucleotide #51.
XX
XX Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KM Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KM scleroderma; hypertension; haemophilia;
KM idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KM dyalipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KM cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS Homo sapiens.
XX
XX US2004058338-A1.
XX
XX 25-MAR-2004.
XX
XX 02-DEC-2002; 2002US-00307817.
XX
XX 03-DEC-2001; 2001US-0336881P.
XX 05-DEC-2001; 2001US-0336820P.
XX 07-DEC-2001; 2001US-0338285P.
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XX 10-DEC-2001; 2001US-0338989P.
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XX 12-DEC-2001; 2001US-0340981P.
XX 12-DEC-2001; 2001US-0341346P.
XX 14-DEC-2001; 2001US-0340390P.
XX 14-DEC-2001; 2001US-0340440P.
XX 14-DEC-2001; 2001US-0340655P.
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XX 17-DEC-2001; 2001US-0341477P.
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XX 28-FEB-2002; 2002US-0360924P.
XX 28-FEB-2002; 2002US-0360964P.
XX 28-FEB-2002; 2002US-0361028P.
XX 28-FEB-2002; 2002US-0361256P.
XX 28-FEB-2002; 2002US-0361264P.
XX 05-MAR-2002; 2002US-0361770P.
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XX 15-MAR-2002; 2002US-0364978P.
XX 15-MAR-2002; 2002US-0365025P.
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XX 16-MAY-2002; 2002US-0381004P.
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XX 29-MAY-2002; 2002US-0384024P.
XX 02-JUL-2002; 2002US-0393332P.
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XX 26-AUG-2002; 2002US-0406353P.
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XX (AGEE/) AGEER M L.
XX (ALSO/) ALSOBROOK J P.
XX (ANDE/) ANDERSON D W.
XX (BERG/) BERGHS C.
XX (BOLD/) BOLDOG F L.
XX (BURG/) BURGESS C E.
XX (CATT/) CATTERTON E.
XX (DIP/) DIPIPPO V A.
XX (EDIN/) EDINGER S R.
XX (EISE/) EISEN A.
XX (EULE/) EULERMAN K.
XX (GANG/) GANGOLI E A.
XX (GERL/) GERLACH V.
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XX (ROTH/) ROTHBERG B G.
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XX (HALV/) HALVORSEN Y.
XX (JIWV/) JI W.
XX (KEKU/) KEKUDA R.
XX (KHRA/) KHRAMTSOV N V.
XX (LARO/) LAROCHELLE W J.
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XX (LILL/) LI L.
XX (MACD/) MACDUGALL J R.
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XX (STON/) STONE D J.
XX (TAUP/) TAUPIER R J.
XX (VERN/) VERNET C A M.
XX (VOSS/) VOSS E Z.
XX (ZHON/) ZHONG M.
XX
XX Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL,
XX Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A,
XX Ellerman K, Gangoli EA, Gerlach V, Gorman L, Rothberg BG,
XX Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV,
XX Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE,
XX Padigaru M, Patturajan M, Pena CE, Peyman JA, Rieger DK,
XX Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA,
XX Stone DJ, Taupier RJ, Vernet CM, Voss EZ, Zhong M;
XX
XX WPI; 2004-268786/25.
XX P-PSDB; ADO42253.
XX
XX New human NOVX polypeptides and nucleic acid molecules, useful for
XX diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
XX atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
XX scleroderma.
XX
XX Claim 20; SEQ ID NO 101; 610pp; English.
XX
XX The invention relates to human NOVX polypeptides and the polynucleotides
XX encoding them. The invention also relates to antibodies specific to the
XX NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
XX useful for manufacturing a medicament for treating a syndrome associated
XX with a human disease, such as a pathology associated with the NOVX

```

CC polypeptide. The sequences are useful for diagnosing, treating or  
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,  
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host  
CC disease, scleroderma, hypertension, hemophilia, idiopathic  
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,  
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated  
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used  
CC as hybridisation probes, in chromosome mapping, in tissue typing, in  
CC preventive medicine or in pharmacogenomics. This sequence represents a  
CC human NOVX polynucleotide of the invention.  
XX  
SQ Sequence 1189 BP, 254 A, 351 C, 327 G, 257 T, 0 U, 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 1189;  
Best Local Similarity 100.0%; Pred. NO. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCATTGCCACTCCATTCTT 20  
DB 702 GCATTGCCACTCCATTCTT 683  
RESULT 11  
AD042258/c  
ID AD042258 standard; cDNA; 1189 BP.  
XX  
AC AD042258;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human NOVX polynucleotide #54.  
XX  
XX Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;  
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;  
KW scleroderma; hypertension; haemophilia;  
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;  
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;  
KW cancer-associated cachexia; multiple sclerosis; fertility.  
XX  
OS Homo sapiens.  
XX  
XX US2004058338-A1.  
PN  
XX  
PD 25-MAR-2004.  
XX  
PF 02-DEC-2002; 2002US-00307817.  
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PR 03-DEC-2001; 2001US-0336881P.  
PR 05-DEC-2001; 2001US-0336820P.  
PR 07-DEC-2001; 2001US-0338285P.  
PR 10-DEC-2001; 2001US-0338318P.  
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PR 11-DEC-2001; 2001US-0339314P.  
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PR 11-DEC-2001; 2001US-0339517P.  
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PR 14-DEC-2001; 2001US-0340565P.  
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PR 20-DEC-2001; 2001US-0342892P.  
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PR 28-FEB-2002; 2002US-0360924P.  
PR 28-FEB-2002; 2002US-0360964P.  
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PR 05-MAR-2002; 2002US-0361770P.  
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PR 23-AUG-2002; 2002US-0405698P.  
PR 26-AUG-2002; 2002US-0406353P.  
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PA (AGEE/) AGE M L.  
PA (ALSO/) ALSOBROCK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BERG/) BERGS C.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CATT/) CATTERTON E.  
PA (DIPI/) DIPIPPO V A.  
PA (EDIN/) EDINGER S R.  
PA (EISE/) EISEN A.  
PA (ELLE/) ELLERMAN K.  
PA (GANG/) GANGOLLI E A.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (ROTH/) ROTHBERG B G.  
PA (GUOX/) GUO X S.  
PA (HERR/) HERRMANN J L.  
PA (HALV/) HALVORSEN Y.  
PA (JIWV/) JI W.  
PA (KEKU/) KERKUDA R.  
PA (KHRA/) KHRAMTSOV N V.  
PA (LARO/) LAROCHELLE W J.  
PA (LEPL/) LEPLEY D M.  
PA (LILL/) LI L.  
PA (MACD/) MACDOUGALL J R.  
PA (MILL/) MILLER C E.  
PA (ORTT/) ORT T.  
PA (PADI/) PADIGARU M.  
PA (PATY/) PATTUDANAN M.  
PA (PENNA/) PENNA C E A.  
PA (PEYM/) PEYMAN J A.  
PA (RIEG/) RIEGER D K.  
PA (ROTH/) ROTHENBERG M E.  
PA (SHEN/) SHENOY S G.  
PA (SMIT/) SMITHSON G.  
PA (SPAD/) SPADERNA S K.  
PA (SPYT/) SPYTEK K A.  
PA (STON/) STONE D J.  
PA (TAUP/) TAUPETER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.

PA (ZHON/) ZHONG M.  
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 PI Agee M., Alsbrook J.P., Anderson D.W., Berghs C., Boldog F.L.,  
 PI Burgess C., Catterton E., DiPippo V.A., Edinger S.R., Eisen A.,  
 PI Ellerman K., Gangoli E.A., Gerlach V., Gorman L., Rothberg B.G., Guo X.S.,  
 PI Herrmann J.L., Halvorsen Y., Ji W., Kekuda R., Khramtsov N.V.,  
 PI Larochele W.J., Lepley D.M., Li L., Macdonald J.R., Miller C.E., Ort T.,  
 PI Padigar M., Parturajan M., Pena CEA., Peyman J.A., Rieger D.K.,  
 PI Rothenberg M.E., Shenoy S.G., Smithson G., Spaderna S.K., Spytek K.A.,  
 PI Stone D.J., Taupier R.J., Vernet C.M., Voas E.Z., Zhong M.,  
 XX  
 DR WPI: 2004-268786/25.  
 DR P-PSDB: ADO42259.  
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 PT New human NOXV polypeptides and nucleic acid molecules, useful for  
 PT diagnosing, preventing or treating NOXV-associated disorder, e.g. cancer,  
 PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or  
 PT scleroderma.  
 XX  
 PS Claim 20; SEQ ID NO 107; 610pp; English.  
 XX  
 CC The invention relates to human NOXV polypeptides and the polynucleotides  
 CC encoding them. The invention also relates to antibodies specific to the  
 CC NOXV polypeptides. The polypeptides, polynucleotides and antibodies are  
 CC useful for manufacturing a medicament for treating a syndrome associated  
 CC with a human disease, such as a pathology associated with the NOXV  
 CC polypeptide. The sequences are useful for diagnosing, treating or  
 CC preventing a NOXV-associated disorder, e.g., cancer, atherosclerosis,  
 CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host  
 CC disease, scleroderma, hypertension, haemophilia, idiopathic  
 CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,  
 CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated  
 CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used  
 CC as hybridisation probes, in chromosome mapping, in tissue typing, in  
 CC preventive medicine or in pharmacogenomics. This sequence represents a  
 CC human NOXV polynucleotide of the invention.  
 XX  
 SO Sequence 1189 BP; 254 A; 351 C; 327 G; 257 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 12; Length 1189;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCATTGCCATCCCATCTT 20  
 Db 702 GCATTGCCATCCCATCTT 683  
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 AC ADO42248;  
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 DT 15-JUL-2004 (first entry)  
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 DE Human NOXV polynucleotide #49.  
 XX  
 KW Human; NOXV; gene; ss; cancer; atherosclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;  
 KW scleroderma; hypertension; haemophilia;  
 KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;  
 KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;  
 KW cancer-associated cachexia; multiple sclerosis; fertility.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004058338-A1.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 02-DEC-2002; 2002US-00307817.  
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PR 03-DEC-2001; 2001US-0336881P.  
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 PR 05-MAR-2002; 2002US-0361770P.  
 PR 05-MAR-2002; 2002US-0362230P.  
 PR 13-MAR-2002; 2002US-0364181P.  
 PR 13-MAR-2002; 2002US-0364238P.  
 PR 15-MAR-2002; 2002US-0364978P.  
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 PR 15-MAY-2002; 2002US-0380981P.  
 PR 16-MAY-2002; 2002US-0381004P.  
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 XX (AGEE/) AGEE M. L.  
 PA (ALSO/) ALBROOK J. P.  
 PA (ANDR/) ANDERSON D. W.  
 PA (BERG/) BERGHs C.  
 PA (BOLD/) BOLDog F. L.  
 PA (BURG/) BURGESS C. E.  
 PA (CAT/) CATTERTON E.  
 PA (DIP/) DIPIPPO V. A.  
 PA (EDIN/) EDINGER S. R.  
 PA (EISE/) EISEN A.  
 PA (ELL/) ELLERMAN K.  
 PA (GANG/) GANGOLI E. A.  
 PA (GERL/) GERLACH V.  
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 PA (ROTH/) ROTHBERG B. G.

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PI Ellerman JI, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV;  
PI Larochele WJ, Lepley DW, Li L, Macdougal JR, Miller CE, Ort T;  
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Rieger DK,  
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA,  
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;  
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DR WPI; 2004-268786/25.  
DR P-PSDB; ADO42249.  
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PT New human NOVX polypeptides and nucleic acid molecules, useful for  
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,  
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or  
PT scleroderma.  
XX  
XX  
PS Claim 20; SEQ ID NO 97; 610pp; English.  
XX  
XX  
CC The invention relates to human NOVX polypeptides and the polynucleotides  
CC encoding them. The invention also relates to antibodies specific to the  
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are  
CC useful for manufacturing a medicament for treating a syndrome associated  
CC with a human disease, such as a pathology associated with the NOVX  
CC polypeptide. The sequences are useful for diagnosing, treating or  
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,  
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host  
CC disease, scleroderma, hypertension, hemophilia, idiopathic  
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyliplidemia,  
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated  
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used  
CC as hybridisation probes, in chromosome mapping, in tissue typing, in  
CC preventive medicine or in pharmacogenomics. This sequence represents a  
CC human NOVX polynucleotide of the invention.  
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SQ Sequence 1191 BP; 252 A; 345 C; 334 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1191;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCATTCTT 20  
DB 722 GCATTGCCACTCCATTCTT 703

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AC ADO42244;  
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KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;  
KW scleroderma; hypertension; haemophilia;  
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;  
KW dyliplidemia; obesity; Crohn's disease; bronchial asthma; anorexia;  
KW cancer-associated cachexia; multiple sclerosis; fertility.  
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OS Homo sapiens.  
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PN US2004058338-A1.  
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PD 25-MAR-2004.  
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PR 17-MAY-2002; 2002US-0381495P.  
PR 28-MAY-2002; 2002US-0383534P.  
PR 28-MAY-2002; 2002US-0383744P.  
PR 29-MAY-2002; 2002US-0383829P.

PR	29-MAY-2002;	2002US-0384024P.
PR	02-JUL-2002;	2002US-0393332P.
PR	06-AUG-2002;	2002US-0401315P.
PR	07-AUG-2002;	2002US-0401788P.
PR	20-AUG-2002;	2002US-0404676P.
PR	23-AUG-2002;	2002US-0405400P.
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PR	26-AUG-2002;	2002US-0406353P.
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PA	(ANDE//	ANDERSON D W.
PA	(BERG//	BERGHS C.
PA	(BOLD//	BOLDG F L.
PA	(BURG//	BURGESS C E.
PA	(CATT//	CATTERTON E.
PA	(DIPI//	DIPPRO V A.
PA	(EDIN//	EDINGER S R.
PA	(EISE//	EISEN A.
PA	(ELLE//	ELLERMAN K.
PA	(GANG//	GANGOLLI E A.
PA	(GERL//	GERLACH V.
PA	(GORM//	GORMAN L.
PA	(ROTH//	ROTHBERG B G.
PA	(GUOX//	GUO X S.
PA	(HERR//	HERRMANN J L.
PA	(HALV//	HALVORSEN Y.
PA	(JTW//	JT W.
PA	(KEKU//	KEKUDA R.
PA	(KHRA//	KHRAMTSOV N V.
PA	(LARO//	LAROCHELLE W J.
PA	(LEPL//	LEPLEY D M.
PA	(LIL//	LI L.
PA	(MACD//	MACDOUGALL J R.
PA	(MILL//	MILLER C E.
PA	(ORTT//	ORT T.
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PA	(PENA//	PENA C E A.
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PA	(RIEG//	RIEGER D K.
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PA	(SHEN//	SHENOY S G.
PA	(SMIT//	SMITHSON G.
PA	(SPAD//	SPADERNA S K.
PA	(SPYT//	SPYTEK K A.
PA	(STON//	STONE D J.
PA	(TAUP//	TAUPIER R J.
PA	(VERN//	VERNET C A M.
PA	(VOSS//	VOSS E Z.
PA	(ZHON//	ZHONG M.
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PI	Agee ML,	Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI	Burgess CE,	Catterton E, Dipippo VA, Edinger SR, Eisen A;
PI	Ellerman K,	Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
PI	Herrmann JL,	Halvorsen Y, Ji W, Kekuda R, Khrantsov NV;
PI	Larochelle WJ,	Lepley DW, Li L, MacDougall JR, Miller CE, Ort T;
PI	Padigar M,	Patturajan M, Pena CE, Peyman JA, Rieger DK;
PI	Rochenberg M,	Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI	Stone DJ,	Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX		
DR	WPI: 2004-268786/25.	
DR	P-PSDB; ADO42245.	
XX		
PT	New human NOXV polypeptides and nucleic acid molecules, useful for	
PT	diagnosing, preventing or treating NOXV-associated disorder, e.g. cancer	
PT	atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or	
PT	scleroderma.	
PS	Claim 20, SEQ ID NO 93; 610P; English.	
XX		

Query Match	100.0%	Score 20;	DB 12;	Length 1191;
Best Local Similarity	100.0%	Pred. NO. 0.1;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db	722 GCATTGCCACATCCCATCTT 703			
Qy	1 GCATTGCCACATCCCATCTT 20			
AD042256/c				
ID	AD042256 standard; cDNA; 1198 BP.			
AC	AD042256;			
XX				
XX	15-JUL-2004 (first entry)			
XX				
DE	Human NOVX polynucleotide #53.			
XX				
KM	Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;			
KM	Alzheimer's disease; Parkinson's disease; graft-versus-host disease;			
KM	scleroderma; hypertension; haemophilia;			
KM	idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;			
KM	dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;			
KM	cancer-associated cachexia; multiple sclerosis; fertility.			
XX				
OS	Homo sapiens.			
XX				
XX	US2004058338-A1.			
PN				
PD	25-MAR-2004.			
XX				
PF	02-DEC-2002; 2002US-00307817.			
XX				
PR	03-DEC-2001; 2001US-0336881P.			
PR	05-DEC-2001; 2001US-0336882P.			
PR	07-DEC-2001; 2001US-0338285P.			
PR	07-DEC-2001; 2001US-0338318P.			
PR	10-DEC-2001; 2001US-0338988P.			
PR	10-DEC-2001; 2001US-0339022P.			
PR	11-DEC-2001; 2001US-0339314P.			
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PR	12-DEC-2001; 2001US-0341346P.			
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PR	17-DEC-2001; 2001US-0341540P.			
PR	18-DEC-2001; 2001US-0341768P.			
PR	20-DEC-2001; 2001US-0342592P.			

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PR 31-DEC-2001; 2001US-0344903P.
PR 01-FEB-2002; 2002US-0353286P.
PR 01-FEB-2002; 2002US-0353288P.
PR 26-FEB-2002; 2002US-0355959P.
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PR 26-FEB-2002; 2002US-0359671P.
PR 27-FEB-2002; 2002US-0359914P.
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PR 28-FEB-2002; 2002US-0360924P.
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PR 05-MAR-2002; 2002US-0362230P.
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PR 23-AUG-2002; 2002US-0405684P.
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PR 26-AUG-2002; 2002US-0406353P.
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PA (AGEE/) AGEE M. L.
PA (ALSO/) ALSOBROOK J. P.
PA (ANDE/) ANDERSON D. W.
PA
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOS F. L.
PA (BURG/) BURGESS C. E.
PA (CATT/) CATTERTON E.
PA (DIP/) DIPPO V. A.
PA (EDIN/) EDINGER S. R.
PA (EISE/) EISEN A.
PA (BLUE/) ELBERMAN K.
PA (GANG/) GANGOLLI E. A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B. G.
PA (GUOX/) GUO X. S.
PA (HERR/) HERRMANN J. L.
PA (HALV/) HALVORSEN Y.
PA (JIMW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N. V.
PA (LARO/) LAROCHELLE W. J.
PA (LEPL/) LEPLEY D. M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J. R.
PA (MILL/) MILLER C. E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENNA/) PENNA C. E. A.
PA (PEYM/) PEYMAN J. A.
PA (RIEG/) RIEGER D. K.
PA (ROTH/) ROTHENBERG M. E.
PA (SHEN/) SHENOY S. G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S. K.

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PA (SPYT/) SPYTEK K. A.
PA (STON/) STONE D. J.
PA (TAUP/) TAUPIER R. J.
PA (VERN/) VERNET C. A. M.
PA (VOSS/) VOSS E. Z.
PA (ZHON/) ZHONG M.
XX
XX Agee M., Alsobrook J.P., Anderson D.W., Bergths C., Boldog F.L.,
PI Burgess C., Catterton E., Dipppo V.A., Edinger S.R., Eisen A.,
PI Ellerman K., Gangolli E., Gerlach V., Gorman L., Rothberg B.G., Guo X.S.;
PI Herrmann J.L., Halvorsen Y., Ji W., Kekuda R., Khramtsov N.V.;
PI Larochele W.J., Lepley D.M., Li L., Macdougall J.R., Miller C.E., Ort T.;
PI Padigaru M., Patturajan M., Pena C.E.A., Peyman J.A., Rieger D.K.,
PI Rothenberg M.E., Shenoy S.G., Smithson G., Spaderna S.K., Spytek K.A.;
PI Stone D.J., Taupier R.J., Vernet C.A.M., Voss E.Z., Zhong M.;
XX
XX WPI: 2004-268786/25.
DR P-PsDB; ADO42257.
DR
XX
XX New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g., cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
XX Claim 20; SEQ ID NO 105; 610pp; English.
XX
XX The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOVX polynucleotide of the invention.
XX
XX Sequence 1198 BP; 251 A; 351 C; 332 G; 264 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 12; Length 1198;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCACTCCCACTTCTT 20
Db 711 GCATTGCCACTCCCACTTCTT 692

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RESULT 15
ADO42250/C
ID ADO42250 standard; cDNA; 1207 BP.
XX
XX ADO42250;
AC
XX 15-JUL-2004 (first entry)
DT
XX
XX Human NOVX polynucleotide #50.
DE
XX
XX Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW scleroderma; hypertension; haemophilia;
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW cancer-associated cachexia; multiple sclerosis; fertility.
XX
XX Homo sapiens.
OS
XX
XX US2004058338-A1.
PN

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XX 25-MAR-2004.
PD 02-DEC-2002; 2002US-00307817.
XX
XX
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XX 03-DEC-2001; 2001US-0336881P.
XX 05-DEC-2001; 2001US-0336820P.
XX 07-DEC-2001; 2001US-0338285P.
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XX 11-DEC-2001; 2001US-0339517P.
XX 12-DEC-2001; 2001US-0339611P.
XX 12-DEC-2001; 2001US-0340981P.
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XX 14-DEC-2001; 2001US-0340565P.
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XX 14-DEC-2001; 2001US-0341144P.
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XX 13-MAR-2002; 2002US-0364238P.
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XX 29-MAY-2002; 2002US-0384024P.
XX 02-JUL-2002; 2002US-0393332P.
XX 06-AUG-2002; 2002US-0401315P.
XX 07-AUG-2002; 2002US-0401788P.
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XX 23-AUG-2002; 2002US-0405400P.
XX 23-AUG-2002; 2002US-0405684P.
XX 23-AUG-2002; 2002US-0405687P.
XX 23-AUG-2002; 2002US-0405698P.
XX 26-AUG-2002; 2002US-0406353P.
XX
XX (AGEB/) AGE E. M. L.
PA (ALSO/) ALSOBROOK J. P.
PA (ANDE/) ANDERSON D. W.
PA (BERG/) BERGH C.
PA (BOLD/) BOLDOS F. L.
PA (BURG/) BURGESS C. E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V. A.
PA (EDIN/) EDINGER S. R.
PA (EISE/) EISEN A.

PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E. A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B. G.
PA (GUOX/) GUO X. S.
PA (HERR/) HERRMANN J. L.
PA (HALV/) HALVORSEN Y.
PA (JIWU/) JI W.
PA (KERA/) KERKUDA R.
PA (KRAM/) KRAMTSOV N. V.
PA (LARO/) LAROCHELLE W. J.
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PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J. R.
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PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENNA/) PENNA C. E. A.
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PA (RIEG/) RIEGER D. K.
PA (ROTH/) ROTHENBERG M. E.
PA (SHEN/) SHENOY S. G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S. K.
PA (SPYT/) SPYTEK K. A.
PA (STON/) STONE D. J.
PA (TAUP/) TAUPIER R. J.
PA (VERN/) VERNET C. A. M.
PA (VOSS/) VOSS E. Z.
PA (ZHON/) ZHONG M.

PI Age ML, Alsbrook JP, Anderson DW, Berghs C, Boldos FL,
PI Bugess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A,
PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG,
PI Herrmann JL, Halvorsen Y, Ji W, Kerkuda R, Kramtssov NV,
PI Larochele WJ, Lepley DM, Li L, Macdougall JR, Miller CE,
PI Padigar M, Patturajan M, Penna CE, Peyman JA, Rieger DK,
PI Rotherberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA,
PI Stone DJ, Taupier RJ, Vernet CM, Voss EZ, Zhong M;
XX
XX WPI: 2004-268786/25.
DR P-PSDB; ADO42251.
XX
XX The invention relates to human NOVX polypeptides and the polynucleotides
XX encoding them. The invention also relates to antibodies specific to the
XX NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
XX useful for manufacturing a medicament for treating a syndrome associated
XX with a human disease, such as a pathology associated with the NOVX
XX polypeptide. The sequences are useful for diagnosing, treating or
XX preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
XX diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
XX disease, scleroderma, hypertension, haemophilia, idiopathic
XX thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
XX obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
XX cachexia, multiple sclerosis or fertility. The nucleic acids may be used
XX as hybridisation probes, in chromosome mapping, in tissue typing, in
XX preventive medicine or in pharmacogenomics. This sequence represents a
XX human NOVX polynucleotide of the invention.
XX
XX Sequence 1207 BP; 258 A; 359 C; 332 G; 258 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 12; Length 1207;
XX Best Local Similarity 100.0%; Pred. No. 0.1;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCATGCACTCCCATCTT 20  
 DB 710 GCATGCACTCCCATCTT 691

RESULT 16  
 ADO42246/c  
 ID ADO42246 standard; cDNA, 1230 BP.  
 XX  
 AC ADO42246;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human NOVX polynucleotide #48.  
 XX

Human; NOVX; gene; 89; cancer; atherosclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;  
 KW scleroderma; hypertension; haemophilia;  
 KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;  
 KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;  
 KW cancer-associated cachexia; multiple sclerosis; fertility.

OS Homo sapiens.  
 XX  
 XX US2004058338-A1.  
 XX  
 XX 25-MAR-2004.  
 PD  
 XX  
 PF 02-DEC-2002; 2002US-00307817.  
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 XX 03-DEC-2001; 2001US-0336881P.  
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 PR 11-DEC-2001; 2001US-0339314P.  
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 PR 05-MAR-2002; 2002US-0362230P.  
 PR 13-MAR-2002; 2002US-0364181P.  
 PR 13-MAR-2002; 2002US-0364238P.  
 PR 15-MAR-2002; 2002US-0364978P.  
 PR 15-MAR-2002; 2002US-0365025P.  
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PR 16-MAY-2002; 2002US-0381004P.  
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 PR 28-MAY-2002; 2002US-0383534P.  
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 PR 29-MAY-2002; 2002US-0383829P.  
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 PR 02-JUL-2002; 2002US-0393333P.  
 PR 06-AUG-2002; 2002US-0401315P.  
 PR 07-AUG-2002; 2002US-0401788P.  
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 PR 23-AUG-2002; 2002US-0405684P.  
 PR 23-AUG-2002; 2002US-0405687P.  
 PR 23-AUG-2002; 2002US-0405698P.  
 PR 26-AUG-2002; 2002US-0406353P.  
 XX

(AGEE/) AGEE M. L.  
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 PA (ANDE/) ANDERSON D. W.  
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 PA (BOLD/) BOLDOS F. L.  
 PA (BURG/) BURGESS C. E.  
 PA (CATT/) CATTERTON E.  
 PA (DIDI/) DIPIPPO V. A.  
 PA (EDIN/) EDINGER S. R.  
 PA (EISE/) EISEN A.  
 PA (ELLE/) ELLERMAN K.  
 PA (GANG/) GANGOLLI E. A.  
 PA (GERL/) GERLACH V.  
 PA (GORM/) GORMAN L.  
 PA (ROTH/) ROTHBERG B. G.  
 PA (GUOX/) GUO X. S.  
 PA (HERR/) HERRMANN J. L.  
 PA (HALV/) HALVORSEN Y.  
 PA (UTWM/) JT W.  
 PA (KERU/) KERUDA R.  
 PA (KHRA/) KHRAMTSOV N. V.  
 PA (LARO/) LAROCHELLE W. J.  
 PA (LEPL/) LEPLLEY D. M.  
 PA (LITL/) LI L.  
 PA (MACD/) MACDOUGALL J. R.  
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 PA (RIEG/) RIEGER D. K.  
 PA (ROTH/) ROTHENBERG M. E.  
 PA (SHEN/) SHENOY S. G.  
 PA (SMIT/) SMITHSON G.  
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 PA (STON/) STONE D. J.  
 PA (TAUP/) TAUPIER R. J.  
 PA (VERN/) VERNET C. A. M.  
 PA (VOSS/) VOSS E. Z.  
 PA (ZHON/) ZHONG M.

XX  
 PI Agee M., Alsebrook J.P., Anderson D.W., Berghs C., Boldog F.L.,  
 PI Burgess C.E., Catterton E., Dipippo V.A., Edinger S.R., Eisen A.,  
 PI Ellerman K., Gangolli E.A., Gerlach V., Gorman L., Rothberg B.G.,  
 PI Hermann J.L., Halvorsen Y., Ji W., Kekuda R., Khrantsov N.V.,  
 PI Larochele W.J., Lepley D.M., Li L., Macdougall J.R., Miller C.E.,  
 PI Padigaru M., Paturajan M., Penna C.E.A., Peyman J.A., Rieger D.K.,  
 PI Rothenberg M.E., Shenoy S.G., Smithson G., Spaderna S.K.,  
 PI Spytsek K.A., Stone D.J., Taupier R.J., Vernet C.A.M., Voss E.Z.,  
 PI Stone D.J., Taupier R.J., Vernet C.A.M., Voss E.Z., Zhong M.,  
 XX  
 DR WPI, 2004-268786/25.  
 DR P-Psdbj, ADO42247.  
 XX  
 PT New human NOVX polypeptides and nucleic acid molecules, useful for  
 diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer.



PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or  
PT scleroderma.  
XX  
XX  
PS Claim 20; SEQ ID NO 95; 610pp; English.  
XX  
CC The invention relates to human NOVX polypeptides and the polynucleotides  
CC encoding them. The invention also relates to antibodies specific to the  
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are  
CC useful for manufacturing a medicament for treating a syndrome associated  
CC with a human disease, such as a pathology associated with the NOVX  
CC polypeptide. The sequences are useful for diagnosing, treating or  
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,  
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host  
CC disease, scleroderma, hypertension, haemophilia, idiopathic  
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,  
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated  
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used  
CC as hybridisation probes, in chromosome mapping, in tissue typing, in  
CC preventive medicine or in pharmacogenomics. This sequence represents a  
CC human NOVX polynucleotide of the invention.  
XX  
SQ Sequence 1230 BP; 259 A; 359 C; 341 G; 271 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 1230;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 1 GCATGCCACCTCCATTCTT 20  
Db 702 GCATGCCACCTCCATTCTT 683  
RESULT 17  
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ID AD042679 standard; cDNA; 1230 BP.  
XX  
AC AD042679;  
XX  
XX 15-JUL-2004 (first entry)  
XX  
XX Human NOVX-related polynucleotide #10.  
XX  
XX Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;  
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;  
KW scleroderma; hypertension; haemophilia;  
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;  
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;  
KW cancer-associated cachexia; multiple sclerosis; fertility.  
XX  
XX Homo sapiens.  
XX  
XX US2004058338-A1.  
XX  
XX 25-MAR-2004.  
XX  
XX 02-DEC-2002; 2002US-00307817.  
XX  
XX 03-DEC-2001; 2001US-0336881P.  
XX 05-DEC-2001; 2001US-0336820P.  
XX 07-DEC-2001; 2001US-0338285P.  
XX 10-DEC-2001; 2001US-0338318P.  
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PR 17-DEC-2001; 2001US-0341540P.  
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PR 31-DEC-2001; 2001US-0344903P.  
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PR 28-FEB-2002; 2002US-0361256P.  
PR 28-FEB-2002; 2002US-0361264P.  
PR 05-MAR-2002; 2002US-0361770P.  
PR 05-MAR-2002; 2002US-0362230P.  
PR 13-MAR-2002; 2002US-0364181P.  
PR 13-MAR-2002; 2002US-0364238P.  
PR 15-MAR-2002; 2002US-0364978P.  
PR 15-MAR-2002; 2002US-0365025P.  
PR 17-APR-2002; 2002US-0373288P.  
PR 15-MAY-2002; 2002US-0380981P.  
PR 16-MAY-2002; 2002US-0381004P.  
PR 17-MAY-2002; 2002US-0381455P.  
PR 28-MAY-2002; 2002US-0383534P.  
PR 28-MAY-2002; 2002US-0383744P.  
PR 29-MAY-2002; 2002US-0383829P.  
PR 29-MAY-2002; 2002US-0384024P.  
PR 02-JUL-2002; 2002US-0393332P.  
PR 06-AUG-2002; 2002US-0401315P.  
PR 07-AUG-2002; 2002US-0401788P.  
PR 20-AUG-2002; 2002US-0404676P.  
PR 23-AUG-2002; 2002US-0405400P.  
PR 23-AUG-2002; 2002US-0405684P.  
PR 23-AUG-2002; 2002US-0405687P.  
PR 23-AUG-2002; 2002US-0405698P.  
PR 26-AUG-2002; 2002US-0406353P.  
XX  
XX (AGEE/) AGEE M L.  
XX (ALSO/) ALSOBOOK J P.  
XX (ANDE/) ANDERSON D W.  
XX (BERG/) BERGHS C.  
XX (BOLD/) BOLDIG F L.  
XX (BURG/) BURGESS C E.  
XX (CATY/) CATTERTON E.  
XX (DIPI/) DIPIPPO V A.  
XX (EDIN/) EDINGER S R.  
XX (ETSE/) EISEN A.  
XX (ELLE/) ELLERMAN K.  
XX (GANG/) GANCOLI E A.  
XX (GERL/) GERLACH V.  
XX (GORM/) GORMAN L.  
XX (ROTH/) ROTHBERG B G.  
XX (GUOX/) GUO X S.  
XX (HERR/) HERRMANN J L.  
XX (HALV/) HALVORSEN Y.  
XX (JIWM/) JI W.  
XX (KEKU/) KEKUDA R.  
XX (KIRA/) KERANTSOV N V.  
XX (LARO/) LAROCHELLE W J.  
XX (LEPL/) LEPLLEY D M.  
XX (LILL/) LI L.  
XX (MACD/) MACDOUGALL J R.  
XX (MILL/) MILLER C E.  
XX (ORTT/) ORT T.  
XX (PADT/) PADIGARU M.  
XX (PATY/) PATYRAJAN M.  
XX (PENNA/) PENNA C B A.  
XX (PEYM/) PEYMAN J A.



```
FT XX /transl_except= (pos:98, .100,aa:AlaLeu)
PN XX MO2004042014-A2.
XX XX
PD 21-MAY-2004.
PF 29-OCT-2003; 2003WO-US034598.
PR 31-OCT-2002; 2002US-00286581.
XX XX
PA (GLAD-) GLADSTONE INST J DAVID.
XX XX
PI Cases S, Stone SJ, Zhou P, Farese RV, Yen CE;
XX XX WPI; 2004-400668/37.
DR P-PsDB; ADO15615.
XX XX
PT New mammalian monoacylglycerol acyltransferase 2 polypeptide, useful for
PT treating cardiovascular disease, hyperlipidemia, obesity, diabetes,
XX cancer, neurological disorders and immunological disorders.
XX XX
PS Example 1; SEQ ID NO 1; 98pp; English.
XX XX
CC The present invention describes a mammalian monoacylglycerol
CC acyltransferase (MGAT, EC 2.3.1.22) polypeptide (Ia) and a diacylglycerol
CC transferase (DGAT, EC 2.3.1.20) polypeptide (Ib) present in other than
CC its naturally occurring environment. Also described: (1) a mammalian
CC polynucleotide (II) present in other than its natural environment
CC encoding a polypeptide that exhibits MGAT and/or DGAT activity; (2) an
CC expression cassette (III) comprising a transcriptional initiation region
CC functional in an expression host, (II) under the transcriptional
CC regulation of the transcriptional initiation region, and transcriptional
CC termination region functional in the expression host; (3) a cell (IV)
CC comprising (III) as a part of an extrachromosomal element or integrated
CC into the genome of a host cell as a result of introducing (III) into the
CC host cell; (4) cellular progeny (V) of (IV); (5) preparing (Ia) and/or
CC (Ib); (6) monoclonal antibody (VI) binding specifically to (Ia) or (Ib);
CC (7) inhibiting (M1) the activity of (Ia) or (Ib); and (8) identifying an
CC agent that inhibits an acyltransferase activity of MGAT2 polypeptide
CC (Ia) and (Ib) have cardiovascular, anorectic, antilipemic, antidiabetic,
CC cytoskeletal and neuroprotective activities. (Ia) can be used for producing
CC in vitro models of diglyceride and/or triglyceride synthesis, and for
CC producing triglyceride compositions which find use in foodstuffs,
CC spreads, cooking materials, feedstocks and in industries for producing
CC chemicals, lubricants and surfactants. (Ia), (Ib) and (VI) are useful for
CC treating disease conditions associated with acylglycerol metabolism.
CC particularly associated with diacylglycerol O-acyltransferase 2 alpha
CC (DGAT2alpha), MGAT1 or MGAT2 activity. The disease conditions include
CC cardiovascular disease, hyperlipidaemia, obesity, diabetes, cancer,
CC neurological disorders and immunological disorders. (II) can be in gene
CC therapy to treat disorders associated with DGAT2alpha, MGAT1 or MGAT2
CC defects, as probes and primers in hybridisation applications (e.g., PCR),
CC for identifying expression patterns in biological specimens, for
CC preparing cell or animal models for DGAT2alpha, MGAT1 or MGAT2 function,
CC for preparing in vitro models for (DGAT2alpha), MGAT1 or MGAT2 function,
CC to generate transgenic host. The present sequence encodes human
CC DGAT2alpha, which is used in the exemplification of the present
CC invention.
XX XX
SQ Sequence 1231 BP; 260 A; 359 C; 341 G; 271 T; 0 U; 0 Other;
```

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Query Match 100.0%; Score 20; DB 12; Length 1231;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Gy 1 GCATTGCACATCCCATCTT 20
Db 705 GCATTGCACATCCCATCTT 683
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RESULT 20
AAD46549/C
ID AAD46549 standard; DNA; 1233 BP.
```

```
XX XX AAD46549;
AC 27-JAN-2003 (first entry)
XX XX
DT Human DGAT/MGAT-related DNA.
XX XX
DE Human; monoacylglycerol acyltransferase; MGAT; hypertriglyceremia; DGAT;
XX diacylglycerol acyltransferase; obesity; anorectic; hypoglycaemic;
XX enzyme; ds.
XX XX
OS Homo sapiens.
XX XX
PN MO200268595-A2.
XX XX
PD 06-SEP-2002.
XX XX
PF 21-FEB-2002; 2002WO-US005474.
XX XX
PR 23-FEB-2001; 2001US-0271307P.
XX XX 26-FEB-2001; 2001US-00794715.
PR 14-JAN-2002; 2002US-00046924.
XX XX
PA (REGC ) UNIV CALIFORNIA.
XX XX
PI Cases S, Stone S, Zhou P, Farese RV, Yen CE;
XX XX WPI; 2002-723199/78.
XX XX
DR WPI; 2002-723199/78.
XX XX
PT New mammalian polynucleotide encoding a polypeptide that exhibits
PT monoacylglycerol and/or diacylglycerol transferase activity, useful for
PT treating a disease condition e.g. hypertriglyceremia or obesity.
XX XX
PS Claim 1; Page 82; 85pp; English.
XX XX
CC The invention relates to a mammalian polynucleotide present in other than
CC its natural environment and encodes a polypeptide that exhibits.
CC monoacylglycerol (MGAT; E.C. 2.3.1.22) and/or diacylglycerol
CC acyltransferase activity (DGAT; E.C. 2.3.1.20). The composition
CC comprising the DGAT2alpha or MGAT1 polynucleotide or polypeptide is
CC useful for treating a disease condition e.g. hypertriglyceremia or
CC obesity. The present sequence is human DGAT/MGAT-related DNA
XX XX
SQ Sequence 1233 BP; 259 A; 360 C; 342 G; 272 T; 0 U; 0 Other;
```

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Query Match 100.0%; Score 20; DB 6; Length 1233;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Gy 1 GCATTGCACATCCCATCTT 20
Db 705 GCATTGCACATCCCATCTT 686
```

```
RESULT 21
AD015631/C
ID AD015631 standard; DNA; 1233 BP.
XX XX
AC AD015631;
XX XX
```

```
DT 12-AUG-2004 (first entry)
XX XX
```

```
DE Human acylglycerol acyltransferase related nucleotide sequence SEQ ID:18.
```

```
XX XX monoacylglycerol acyltransferase; MGAT; EC 2.3.1.22;
XX XX diacylglycerol transferase; DGAT; EC 2.3.1.20; enzyme; cardiovascular;
XX XX anorectic; antilipemic; antidiabetic; cytoskeletal; neuroprotective;
XX XX diglyceride; triglyceride; acylglycerol metabolism;
XX XX cardiovascular disease; hyperlipidaemia; obesity; diabetes; cancer;
XX XX neurological disorder; immunological disorder; gene therapy; human; gene;
XX XX ds.
```

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OS Homo sapiens.
```

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XX WO2004042014-A2.
XX
XX
XX 21-MAY-2004.
XX
XX 29-OCT-2003; 2003WO-US034596.
XX
XX 31-OCT-2002; 2002US-00266581.
XX
XX (GLAD-) GLADSTONE INST J DAVID.
XX
XX Cases S, Stone SJ, Zhou P, Farese RV, Yen CE;
XX
XX WPI; 2004-400668/37.
XX
XX New mammalian monoacylglycerol acyltransferase 2 polypeptide, useful for
XX treating cardiovascular disease, hyperlipidemia, obesity, diabetes,
XX cancer, neurological disorders and immunological disorders.
XX
XX Disclosure; SEQ ID NO 16; 98pp; English.
XX
XX The present invention describes a mammalian monoacylglycerol
XX acyltransferase (MGAT, EC 2.3.1.22) polypeptide (1a) and a diacylglycerol
XX transferase (DGAT, EC 2.3.1.20) polypeptide (1b) present in other than
XX its naturally occurring environment. Also described: (1) a mammalian
XX polynucleotide (1i) present in other than its natural environment
XX encoding a polypeptide that exhibits MGAT and/or DGAT activity; (2) an
XX expression cassette (1ii) comprising a transcriptional initiation region
XX functional in an expression host, (1i) under the transcriptional
XX regulation of the transcriptional initiation region; (3) a cell (1iv)
XX comprising (1ii) as a part of an extrachromosomal element or integrated
XX into the genome of a host cell as a result of introducing (1ii) into the
XX host cell; (4) cellular progeny (iv) of (1v); (5) preparing (1a) and/or
XX (1b); (6) monoclonal antibody (vi) binding specifically to (1a) or (1b);
XX (7) inhibiting (mi) the activity of (1a) or (1b); and (8) identifying an
XX agent that inhibits an acyltransferase activity of MGAT2 polypeptide.
XX (1a) and (1b) have cardiovascular, anorectic, antidiabetic, antidiabetic,
XX cytosolic and neuroprotective activities. (1a) can be used for producing
XX in vitro models of diglyceride and/or triglyceride synthesis, and for
XX producing triglyceride compositions which find use in foodstuffs,
XX spreads, cooking materials, feedstocks and in industries for producing
XX chemicals, lubricants and surfactants. (1a), (1b) and (vi) are useful for
XX treating disease conditions associated with acylglycerol metabolism,
XX particularly associated with diacylglycerol O-acyltransferase 2 alpha
XX (DGAT2alpha), MGAT1 or MGAT2 activity. The disease conditions include
XX cardiovascular disease, hyperlipidemia, obesity, diabetes, cancer,
XX neurological disorders and immunological disorders. (1i) can be in gene
XX therapy to treat disorders associated with DGAT2alpha, MGAT1 or MGAT2
XX defects, as probes and primers in hybridisation applications (e.g., PCR),
XX for identifying expression patterns in biological specimens, for
XX preparing cell or animal models for DGAT2alpha, MGAT1 or MGAT2 function,
XX for preparing in vitro models for (DGAT2alpha), MGAT1 or MGAT2 function,
XX to generate transgenic host. The present sequence represents a human
XX acylglycerol acyltransferase related nucleotide sequence, which is used
XX in the exemplification of the present invention.
XX
XX
XX Sequence 1233 BP; 259 A; 360 C; 342 G; 272 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 12; Length 1233;
XX Best Local Similarity 100.0%; Pred. No. 0.1;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCATTGCCACTCCCATTTCTT 20
XX |||||||||||||||||||
XX DB 705 GCATTGCCACTCCCATTTCTT 686
XX
XX
XX RESULT 22
XX AA233556/c
XX ID AA233556 standard; cDNA; 1303 BP.
XX
XX AA233556;
XX AC

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XX 08-DEC-1999 (first entry)
XX
XX Human breast tumour-associated EST 16.
XX
XX Expressed sequence tag; EST; human; breast; cancer; cytostatic;
XX KW medicaments; gene therapy; treatment; fat metabolism; ss.
XX
XX Homo sapiens.
XX
XX DE19813835-A1.
XX
XX 23-SEP-1999.
XX
XX 20-MAR-1998; 98DE-01013835.
XX
XX 20-MAR-1998; 98DE-01013835.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX
XX WPI; 1999-528979/45.
XX
XX P-PSDB; AAY48474.
XX
XX Human nucleic acid sequences and protein products from normal breast
XX PT tissue, useful for breast cancer therapy.
XX
XX Claim 1a; 103; 206pp; German.
XX
XX This invention describes novel human nucleic acid sequences from normal
XX breast tissue which have cytostatic activity. The nucleic acid sequences
XX can be used to produce and isolate full-length gene sequences. They can
XX be used to express proteins, which can be used as tools to find an
XX activity against breast cancer. The sequences can be used in sense or
XX CC antisense form. They are especially useful for medicaments for gene
XX CC therapy to treat breast cancer and for treating illnesses associated with
XX CC fat metabolism. AA233541-233610 represent expressed sequence tags
XX
XX
XX Sequence 1303 BP; 292 A; 337 C; 352 G; 322 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 1303;
XX Best Local Similarity 100.0%; Pred. No. 0.1;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCATTGCCACTCCCATTTCTT 20
XX |||||||||||||||||||
XX DB 151 GCATTGCCACTCCCATTTCTT 132
XX
XX
XX RESULT 23
XX ADR26804
XX ID ADR26804 standard; DNA; 1510 BP.
XX
XX ADR26804;
XX
XX 21-OCT-2004 (first entry)
XX
XX Breast cancer prognosis marker #2665.
XX
XX de; breast cancer; prognosis; gene expression; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2004065545-A2.
XX
XX 05-AUG-2004.
XX
XX 15-JAN-2004; 2004WO-US001100.
XX
XX 15-JAN-2003; 2003US-00342887.
XX
XX
XX
XX

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PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 XX  
 XX Van't Veer LJ, He Y;  
 DR WPI; 2004-593473/57.  
 XX  
 PT Classifying a breast cancer patient according to prognosis comprises  
 PT determining the similarity between the level of expression of each of  
 PT five genes in a cell sample taken from patient, to control levels.  
 XX  
 XX Disclosure; SEQ ID NO 2665; 226pp; English.  
 XX  
 CC The invention relates to a method of classifying a breast cancer patient  
 CC according to prognosis by determining the similarity between the level of  
 CC expression of each of five genes for which markers are listed in the  
 CC specification, in a cell sample taken from the breast cancer patient, to  
 CC control levels of expression for each respective five genes to obtain a  
 CC patient similarity value. The methods are useful for classifying a breast  
 CC cancer patient according to prognosis, kits and computer program products  
 CC are useful for data analysis using the diagnostic, prognostic and  
 CC statistical methods of the invention. This sequence corresponds to a  
 CC marker used in the method of the invention.  
 CC  
 SQ Sequence 1510 BP; 375 A; 398 C; 393 G; 344 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 13; Length 1510;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GCATTGCCACTCCCATCTT 20  
 Db 1491 GCATTGCCACTCCCATCTT 1510  
 RESULT 24  
 ABL53628/c  
 ID ABL53628 standard; cDNA; 1543 BP.  
 XX  
 AC ABL53628;  
 XX  
 DT 17-JUN-2002 (first entry)  
 XX  
 DE Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) cDNA.  
 XX  
 KW BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;  
 KW cytosolic; differential expression; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 228..1394  
 FT /\*tag= a  
 FT /product= "BSTP-ECG1"  
 XX  
 PN WO200208260-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 26-JUL-2001; 2001WO-US023439.  
 XX  
 PR 26-JUL-2000; 2000US-0220967P.  
 PR 06-DEC-2000; 2000US-0251669P.  
 XX  
 PA (STRD ) UNIV STANFORD.  
 PA (GENO-) APPLIED GENOMICS INC.  
 XX  
 PI Borestein D, Brown PO, Petou C, Rose D, Seitz R;  
 DR WPI; 2002-315251/35.  
 DR P-PSDB; ABB75677.  
 XX  
 PT Novel substantially purified polypeptide encoded by breast protein-

PT eukaryotic conserved gene 1, useful for diagnosing, treating or  
 PT preventing breast cancer, and for classifying cancer.  
 XX  
 XX Disclosure; Fig 1D; 127pp; English.  
 PS  
 CC The present sequence is that of a BSTP-ECG1 (breast protein-eukaryotic  
 CC conserved gene 1) cDNA sequence, encoding a 388-amino acid protein (see  
 CC ABB75677). The cDNA corresponds to a 1.5 kb mRNA isoform detected in  
 CC liver tumour-derived HepG2 cells (ATCC HB-8065), colon tumour-derived  
 CC COLO205 cells (ATCC CCL-222) and breast adenocarcinoma-derived MCF-7  
 CC cells (ATCC HTB-22) using Northern blotting. Multiple isoforms of BST-  
 CC ECG1 mRNA are predicted resulting from alternative 3' processing. BSTP-  
 CC ECG1 is differentially expressed among breast tumours, making it useful  
 CC for the diagnosis, treatment, prevention, prognosis and classification of  
 CC cancer, especially breast cancer, and a target for therapeutic  
 CC intervention. The invention provides BSTP-ECG1 polypeptides and  
 CC polynucleotides, expression vectors, host cells, antibodies, agonists and  
 CC antagonists. It also provides methods for treating or preventing  
 CC disorders of cell proliferation, particularly breast cancer, by  
 CC administering a polypeptide, polynucleotide or antibody of the invention.  
 CC Also provided are methods of classifying diseases, particularly breast  
 CC cancer, by detecting expression of BSTP-ECG1 or a polynucleotide encoding  
 CC it, and of providing diagnostic, prognostic and/or predictive information  
 CC for a patient based on the detection and/or measurement of BSTP-ECG1 or a  
 CC polynucleotide encoding BSTP-ECG1. Since BST-ECG1 mRNA can be detected in  
 CC a variety of tumour-derived cell lines, these methods may also be  
 CC applicable to additional tumour types  
 CC  
 SQ Sequence 1543 BP; 321 A; 452 C; 441 G; 329 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 1543;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GCATTGCCACTCCCATCTT 20  
 Db 925 GCATTGCCACTCCCATCTT 906  
 RESULT 25  
 AAA37103/c  
 ID AAA37103 standard; cDNA; 1570 BP.  
 XX  
 AC AAA37103;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Human PRO1433 (UNQ738) cDNA sequence SEQ ID NO:291.  
 XX  
 KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200012708-A2.  
 XX  
 PD 09-MAR-2000.  
 XX  
 PF 01-SEP-1999; 99WO-US020111.  
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 PR 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 09-SEP-1998; 98US-0099536P.  
 PR 09-SEP-1998; 98US-0099596P.  
 PR 09-SEP-1998; 98US-0099598P.  
 PR 09-SEP-1998; 98US-0099602P.  
 PR 09-SEP-1998; 98US-0099642P.  
 PR 10-SEP-1998; 98US-0099741P.  
 PR 10-SEP-1998; 98US-0099754P.

PR	10-SEP-1998	98US-009376733
PR	10-SEP-1998	98US-009379722
PR	10-SEP-1998	98US-009380282
PR	10-SEP-1998	98US-009381222
PR	10-SEP-1998	98US-009381522
PR	10-SEP-1998	98US-009381622
PR	10-SEP-1998	98US-009381822
PR	10-SEP-1998	98US-010033682
PR	15-SEP-1998	98US-010035302
PR	16-SEP-1998	98US-010055422
PR	16-SEP-1998	98US-010066272
PR	16-SEP-1998	98US-010066122
PR	16-SEP-1998	98US-010066222
PR	16-SEP-1998	98US-010066422
PR	17-SEP-1998	98US-010066322
PR	17-SEP-1998	98US-010066422
PR	17-SEP-1998	98US-010071122
PR	17-SEP-1998	98US-010071122
PR	17-SEP-1998	98US-010094922
PR	18-SEP-1998	98US-010094822
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PR	18-SEP-1998	98US-010101422
PR	18-SEP-1998	98US-010106822
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PR	23-SEP-1998	98US-010147122
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PR	30-SEP-1998	98US-010257122
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PR	07-OCT-1998	98US-010331122
PR	07-OCT-1998	98US-010331122
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PR	20-OCT-1998	98US-010458722
PR	20-OCT-1998	98US-010500022
PR	20-OCT-1998	98US-010500222
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PR	17-NOV-1998	98US-0108787P
PR	17-NOV-1998	98US-0108788P
PR	17-NOV-1998	98US-0108801P
PR	17-NOV-1998	98US-0108802P
PR	17-NOV-1998	98US-0108806P
PR	17-NOV-1998	98US-0108807P
PR	17-NOV-1998	98US-0108867P
PR	17-NOV-1998	98US-0108925P
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PR	18-NOV-1998	98US-0108850P
PR	18-NOV-1998	98US-0108851P
PR	18-NOV-1998	98US-0108852P
PR	18-NOV-1998	98US-0108853P
PR	18-NOV-1998	98US-0108904P

(GETH ) GENENTECH INC.

Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

WPI; 2000-237871/20.

P-PSDB; AAY99421.

New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.

Claim 2; Fig 163; 773pp; English.

CC AAAA7022 to AAAA7144 encode the new isolated human transmembrane,  
CC receptor or secreted PRO polypeptides given in AA499340 to AA499462. The  
CC transmembrane and receptor PRO proteins can be used for screening of  
CC potential peptide or small molecule inhibitors of the relevant  
CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
CC encoding them have various industrial applications, including uses as  
CC pharmaceutical and diagnostic agents. AAAA7145 to AAAA7330 represent  
CC primers and hybridisation probes used in the isolation of the PRO  
CC polypeptides from the present invention

SQ Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

Query Match	100.0%;	Score 20;	DB 3;	Length 1570;
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Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Dy 1 GCATTGCCACTCCCATTCCTT 20  
|||  
Dd 882 GCATTGCCACTCCCATTCCTT 863

RESULT 26  
AAF54409/C

ID AAF54409 standard; DNA; 1570 BP.  
XX AAF54409;  
AC  
XX  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Primer #86 used in the identification of proteins.  
XX  
KM Secreted; transmembrane; gene therapy; ss.  
XX  
XX Unidentified.  
OS  
XX WO200078961-A1.  
XX  
XX PD 28-DEC-2000.  
XX  
XX PF 18-FEB-2000; 2000WO-US004342.  
XX  
XX PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
XX  
XX PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Bostein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
PI Williams PM, Wood WI;  
DR WPI; 2001-071395/08.  
XX  
XX PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
PT useful as hybridization probes, in chromosome and gene mapping and gene  
PT therapy.  
XX  
XX PS Example 84; Page 457; 787pp; English.  
XX  
XX CC The present invention relates to secreted and transmembrane proteins.  
CC These proteins and the DNA encoding them may be used as hybridization  
CC probes, in chromosome and gene mapping and in the generation of anti-  
CC sense RNA and DNA. They may also be used to generate either  
CC transgenic animals or knockout animals which are in turn useful for  
CC development and screening of therapeutically useful reagents. The nucleic  
CC acids may also be used in gene therapy  
XX  
XX SQ Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 20; DB 4; Length 1570;  
XX Best Local Similarity 100.0%; Pred. No. 0.1;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GCATGCCACTCCCATCTT 20  
DB 882 GCATGCCACTCCCATCTT 863

KM PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;  
KM dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KM blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KM adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;  
KM PCR primer.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200168848-A2.  
XX  
XX PD 20-SEP-2001.  
XX  
XX PF 28-FEB-2001; 2001WO-US006520.  
XX  
XX PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 06-MAR-2000; 2000US-0186968P.  
PR 14-MAR-2000; 2000US-0189320P.  
PR 14-MAR-2000; 2000US-0189328P.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 21-MAR-2000; 2000US-0190828P.  
PR 21-MAR-2000; 2000US-0191007P.  
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PR 21-MAR-2000; 2000US-0191314P.  
PR 28-MAR-2000; 2000US-0192655P.  
PR 29-MAR-2000; 2000US-0193032P.  
PR 29-MAR-2000; 2000US-0193053P.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 04-APR-2000; 2000US-0194449P.  
PR 04-APR-2000; 2000US-0194647P.  
PR 11-APR-2000; 2000US-0195975P.  
PR 11-APR-2000; 2000US-0196008P.  
PR 11-APR-2000; 2000US-0196187P.  
PR 11-APR-2000; 2000US-0196690P.  
PR 18-APR-2000; 2000US-0196820P.  
PR 18-APR-2000; 2000US-0198121P.  
PR 18-APR-2000; 2000US-0198585P.  
PR 25-APR-2000; 2000US-0199397P.  
PR 25-APR-2000; 2000US-0199550P.  
PR 25-APR-2000; 2000US-0199654P.  
PR 03-MAY-2000; 2000US-0201516P.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
XX  
XX PA (GETH ) GENENTECH INC.  
XX  
XX PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX DR WPI; 2001-602746/68.  
XX P-Psdb; AAU29191.  
XX  
XX PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
XX presence of tumors, such as prostate and breast tumors, in mammals and to  
XX screen for modulators of the compounds.  
XX  
XX PS Claim 2; Fig 335; 774pp; English.  
XX  
XX CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
XX primers for PRO polypeptides of the invention. The sequences of the  
XX invention can be used to detect the presence of a tumour in a mammal by  
XX comparing the level of expression of a PRO polypeptide in a test sample  
XX of cells from the animal and a control sample of normal cells, whereby a

CC higher level of expression in the test sample indicates the presence of a  
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
CC blood, when contacted with it. A specific polypeptide can be used to  
CC stimulate the proliferation or differentiation of chondrocyte cells. The  
CC PRO proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders  
SQ

Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 1570;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
Db 882 GCATTGCCACTCCCATCTT 863

RESULT 28  
ACa89542/c  
ID Aca89542 standard; cDNA; 1570 BP.  
XX  
AC Aca89542;  
XX  
DT 09-JUL-2003 (first entry)  
XX  
XX cDNA encoding human PRO polypeptide #168.  
DE  
XX  
XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW Chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;  
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;  
KW tumour necrosis factor-alpha; proliferation; differentiation;  
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;  
KW arthritis; cystostatic; antiarthritic; osteopathic; gene therapy; gene;  
XX 86.  
XX  
OS Homo sapiens.  
XX  
PN US2003036141-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 01-JUL-2002; 2002US-00187597.  
XX  
PR 18-SEP-1997; 97US-0059263P.  
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PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
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PR 28-OCT-1997; 97US-0063540P.  
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PR 31-OCT-1997; 97US-0063706P.  
PR 31-OCT-1997; 97US-0064103P.  
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PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
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PR 10-MAR-1998; 98US-0077450P.  
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PR 11-MAR-1998; 98US-0077649P.

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PR 24-JUN-1998; 98US-0090435P.  
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PR 26-AUG-1998; 98US-0097952P.  
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PR 26-AUG-1998; 98US-0097974P.  
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PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
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PR 02-SEP-1998; 98US-0098843P.  
PR 09-SEP-1998; 98US-0099602P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099812P.  
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PR 16-SEP-1998; 98US-0101751P.  
PR 16-SEP-1998; 98WO-US019330.  
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PR 30-SEP-1998; 98US-0102570P.  
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PR 01-OCT-1998; 98US-0102687P.  
  
Query Match 100.0%; Score 20; DB 8; Length 1570;  
Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Gaps 0;  
Matches 20; Conservative 0; Indels 0; Gaps 0;  
  
Qy 1 GCATTGCCACTCCCATCTT 20  
Db 882 GCATTGCCACTCCCATCTT 863  
  
RESULT 29  
ACA73552/C  
ID ACA73552 standard; cDNA, 1570 BP.  
XX  
AC ACA73552;  
XX  
DT 01-JUN-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein (PRO) cDNA #168.  
XX  
KW Human; se; gene; secreted protein; transmembrane protein; PRO; tumour;  
KW proliferation; differentiation; chondrocyte cells;  
XX tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.  
OS Homo sapiens.  
XX  
PN US2003036146-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 02-JUL-2002; 2002US-00187603.  
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PR 07-OCT-1998; 98WO-US021141.  
PR 06-NOV-1998; 98US-00187368.  
PR 01-DEC-1998; 98WO-US025108.  
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PR 03-MAR-1999; 99US-00254311.  
PR 08-MAR-1999; 99WO-US005028.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012352.  
PR 25-AUG-1999; 99US-00380137.  
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PR 30-DEC-1999; 99WO-US031374.  
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PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.



PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 26-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 08-NOV-2000; 2000US-00709238.  
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PR 01-DEC-2000; 2000WO-US032678.  
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PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854288.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021056.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 30-JUL-2001; 2001US-00918585.  
PR 06-AUG-2001; 2001US-00924419.  
PR 13-AUG-2001; 2001US-00929404.  
PR 16-AUG-2001; 2001US-00931836.  
PR 28-AUG-2001; 2001US-00941932.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 04-SEP-2001; 2001WO-US046374.  
PR 15-JAN-2002; 2002US-00052586.  
XX  
PA (GETH ) GENENTECH INC.  
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski P, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI: 2003-332039/31.  
DR P-PSDB; AB067573.  
XX  
XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,  
PT in tissue typing, and in chromosome identification.  
XX  
XX Claim 2; Fig 335; 706pp; English.  
XX  
XX The invention discloses human nucleic acids encoding secreted and  
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that  
CC specifically binds to the PRO polypeptide, a method for stimulating the  
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by  
CC contacting the blood a PRO polypeptide, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells by contacting the  
CC cells with a PRO polypeptide, a method for detecting the presence of a  
CC tumour in a mammal and an oligonucleotide probe derived from any of the  
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,  
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in  
CC preparing PRO polypeptides by recombinant techniques and in gene therapy  
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful  
CC as molecular weight markers for protein electrophoresis purposes, for  
CC chromosome identification, as chromosome markers, as therapeutic agents,  
CC for stimulating the release of TNF-alpha from human blood, for  
CC stimulating the proliferation or differentiation of chondrocytes and  
CC detecting the presence of a tumour. The PRO polypeptides and nucleic  
CC acids may also be used diagnostically for tissue typing. The sequences  
CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO  
CC polypeptides of the invention  
XX  
SQ Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 1570;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCACTCCCATCTT 20  
Db .882 GCATTGCCACTCCCATCTT 863  
RESULT 31  
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ID ACA66701 standard; cDNA; 1570 BP.  
XX  
XX ACA66701;  
XX  
XX 23-JUN-2003 (first entry)  
XX  
XX cDNA encoding human PRO protein #168.  
XX  
XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;  
XX liver; PRO; gene therapy; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2003036137-A1.  
XX  
XX 20-FEB-2003.  
XX  
XX 27-JUN-2002; 2002US-00184640.  
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XX 26-JUN-1998; 98US-00105413.  
XX 16-SEP-1998; 98WO-US019330.  
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XX 25-AUG-1999; 99US-00380137.  
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XX 01-SEP-1999; 99WO-US020111.  
XX 15-SEP-1999; 99WO-US021090.  
XX 18-OCT-1999; 99US-00403297.  
XX 12-NOV-1999; 99US-00423844.  
XX 01-DEC-1999; 99WO-US028301.  
XX 02-DEC-1999; 99WO-US028551.  
XX 30-DEC-1999; 99WO-US031274.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 18-FEB-2000; 2000WO-US004342.  
XX 22-FEB-2000; 2000WO-US004414.  
XX 24-FEB-2000; 2000WO-US005004.  
XX 01-MAR-2000; 2000WO-US005601.  
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XX 15-MAR-2000; 2000WO-US006884.  
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XX 22-MAY-2000; 2000WO-US014042.  
XX 30-MAY-2000; 2000WO-US014941.  
XX 02-JUN-2000; 2000WO-US015264.  
XX 28-JUL-2000; 2000WO-US020710.  
XX 22-AUG-2000; 2000US-00644848.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 18-SEP-2000; 2000US-00664610.  
XX 18-SEP-2000; 2000US-00665350.  
XX 08-NOV-2000; 2000US-00709238.  
XX 08-NOV-2000; 2000WO-US030952.  
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PR 29-AUG-2001; 2001US-00942099.  
PR 04-SEP-2001; 2001US-00946374.  
PR 15-JAN-2002; 2002US-00052586.

XX (GETH ) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX

DR MPI; 2003-342038/32.

XX F-PSDB; AB080601.

PT Three hundred and five nucleic acids encoding secreted and transmembrane  
PT PRO polypeptides, useful for the diagnosis, prevention and/or treatment  
PT of tumors, such as adrenal, lung, colon, breast, prostate, rectal,  
PT cervical or liver tumors.

XX Claim 2; Fig 335; 708bp; English.

XX The invention relates to three hundred and five nucleic acids encoding  
XX PRO polypeptides (secreted and transmembrane). Methods and compositions  
CC of the present invention are useful for the diagnosis, prevention and/or  
CC treatment of tumors, such as adrenal, lung, colon, breast, prostate,  
CC rectal, cervical or liver tumors. The PRO polypeptides are also useful  
CC as molecular weight markers, or for chromosome identification. The PRO  
CC genes are useful as hybridization probes, or for screening libraries of  
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
CC therapy, particularly for replacing a defective gene. The present  
CC sequence represents a cDNA encoding a human PRO polypeptide of the  
XX invention

CC Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 20; DB 8; Length 1570;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCATTCTT 20  
Db 882 GCATTGCCACTCCATTCTT 863

RESULT 32

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ID ACF20276 standard; cDNA; 1570 BP.

XX ACF20276;

XX 18-SEP-2003 (first entry)

DE Human secreted polypeptide PRO1433-encoding cDNA, SEQ ID NO:335.

XX KW Human; PRO; secreted protein; transmembrane protein;  
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
XX chondrocyte; proliferation; differentiation; cartilage disorder;  
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;

KW antiarthritic; vulnery; gene therapy; gene; ss.  
XX Homo sapiens.  
OS US2003040063-A1.  
XX PD 27-FEB-2003.  
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Query Match 100.0%; Score 20; DB 8; Length 1570;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCATTGCCACTCCCATCTT 20
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RESULT 33
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AC  ACF19662;
XX  17-SEP-2003 (first entry)
XX  Human secreted polypeptide PRO1433-encoding cDNA, SEQ ID NO:335.
DE  Human secreted polypeptide PRO1433-encoding cDNA, SEQ ID NO:335.
XX  Human; PRO; secreted protein; transmembrane protein;
XX  extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW  chondrocyte; proliferation; differentiation; cartilage disorder;
KW  bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW  adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW  liver; drug screening; transgenic animal; genetic analysis;
KW  antihistatic; vulnery; gene therapy; gene; ss.
XX  Homo sapiens.
OS  Homo sapiens.
XX  US2003040064-A1.
EN  27-FEB-2003.
XX  PD

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XX 26-JUN-2002; 2002US-00183008.  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID ACD21950 standard; cDNA, 1570 BP.

ACD21950;

DT 25-AUG-2003 (first entry)

DE Human secreted/transmembrane protein (PRO) cDNA #168.

KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;  
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX Homo sapiens.

OS US2003027267-A1.

PD 06-FEB-2003.

PF 19-JUN-2002; 2002US-00175739.

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Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 882 GCATTGCCATCCCATCTT 863

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ID ACF13115 standard; cDNA; 1570 BP.

XX ACF13115;

XX 13-SEP-2003 (first entry)

DE Human secreted polypeptide PRO1433-encoding cDNA, SEQ ID NO:335.

XX Human; PRO; secreted protein; transmembrane protein;  
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antithrptic; vulnerary; gene therapy; gene; ss.

XX Homo sapiens.

OS US2003036160-A1.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-00188781.

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Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;  
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Qy 1 GCATTGCCACTCCCATTCCTT 20  
Db 882 GCATTGCCACTCCCATTCCTT 863

## RESULT 36

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ID ACD25218 standard; cDNA; 1570 BP.

XX ACD25218;  
XX

DT 30-AUG-2003 (first entry)  
XX

DE Human secreted/transmembrane protein (PRO) cDNA #168.  
XX

XX Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX Homo sapiens.  
XX

XX US2003044925-A1.  
XX

XX 06-MAR-2003.  
PD

PF 25-JUN-2002; 2002US-00180560.  
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XX 18-SEP-1997; 97US-0059263P.  
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Best Local Similarity 100.0%; Pred. No. 0.1; Indels 0; Gaps 0;
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Db 882 GCATTGCCACTCCCATCTT 863

RESULT 37
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ID ACF00267 standard; cDNA; 1570 BP.
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AC ACF00267;
XX
DT 19-SEP-2003 (first entry)
XX
DE Human secreted polypeptide PRO1433-encoding cDNA, SEQ ID NO:335.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054474-A1.
XX
BD 20-MAR-2003.
XX
PF 22-JUN-2002; 2002US-00201530.
XX
PR 22-JUN-1998; 98US-0090254P.
PR 02-JUN-1998; 99MO-US012252.
PR 25-AUG-1998; 99US-00380137.
PR 28-FEB-2001; 2001WO-US006520.
PR 15-JAN-2002; 2002US-00052586.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Chen J, Deenoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-503631/47.
XX
P-PSDB; ABR78394.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, or for preparing a medicament for treating a condition
PT that is responsive to the PRO polypeptide or anti-PRO antibody.
XX
PS Claim 2; Fig 335; 700bp; English.
XX
CC The invention relates to human PRO secreted/transmembrane polypeptides
CC (ABR7227-ABR78531) and nucleic acids encoding them (ACF00100-00404). The
CC invention also relates to sequences at least 80% identical to the PRO
CC nucleic acid and polypeptide sequences of the invention, recombinant
CC vectors and host cells comprising a PRO nucleic acid, a method for the

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DT 06-AUG-2003 (first entry)  
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KW Human; ss; gene therapy; tumour necrosis factor alpha; TNF-alpha;  
KW chondrocyte stimulation; tumour; tissue typing; gene.  
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OS Homo sapiens.  
XX  
PN US2003032101-A1.  
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BD 13-FEB-2003.  
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PF 17-JUN-2002; 2002US-00173695.  
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AC 18309;

DT 26-AUG-2003 (first entry)

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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.

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XX 20-FEB-2003.

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 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
 KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
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XX DT 09-JUL-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO1433 cDNA.

KM Human; ss; gene therapy; chondrocyte stimulation; TNF-alpha release;  
KW chondrocyte proliferation; chondrocyte differentiation; tumour detection;  
KM tissue typing; gene.

XX Homo sapiens.

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DT 11-AUG-2003 (first entry)
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KW Human; gene; ss; secreted and transmembrane protein; PRO;
KW Chromosome mapping; gene mapping; gene therapy;
KW Tumour necrosis factor alpha; TNF-alpha; chondrocyte; tumour.
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OS Homo sapiens.
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RESULT 44

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DT 13-AUG-2003 (first entry)

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XX

XX Human; secreted and transmembrane protein; PRO; gene therapy;

KM Chondrocyte stimulator; chromosome mapping; gene mapping;

KM transgenic animal; knockout animal; tissue typing;

KM Chondrocyte proliferation; chondrocyte differentiation;

KM tumour necrosis factor-alpha stimulation; TNF-alpha stimulation; gene;

KM

XX

OS Homo sapiens.

XX

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Post-processing: Listing first 100 summaries

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C 73	16	80.0	127946 8 AC104473	AC104473 Oryza sat
C 74	16	80.0	128559 8 CNS08C81	AL731878 Oryza sat
C 75	16	80.0	130965 8 AC026773	AC026773 Homo sapi
C 76	16	80.0	133759 8 OSJN00289	AL731642 Oryza sat
C 77	16	80.0	136393 2 AC151700	AC151700 Gallus ga
C 78	16	80.0	140026 9 AC005840	AC005840 Homo sapi
C 79	16	80.0	140070 2 AC142487	AC142487 Rattus no
C 80	16	80.0	142772 2 AP004184	AP004184 Oryza sat
C 81	16	80.0	142772 10 AL928683	AL928683 Mouse DNA
C 82	16	80.0	143046 8 AP004191	AP004191 Oryza sat
C 83	16	80.0	144563 8 CNS08C7P	AL731740 Oryza sat
C 84	16	80.0	150137 8 AC135226	AC135226 Oryza sat
C 85	16	80.0	152884 9 AC138625	AC138625 Homo sapi
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C 87	16	80.0	157462 2 AC130459	AC130459 Homo sapi
C 88	16	80.0	157838 9 HUAC004626	AC004626 Homo sapi
C 89	16	80.0	158420 9 AC137788	AC137788 Homo sapi
C 90	16	80.0	159832 2 AC110764	AC110764 Homo sapi
C 91	16	80.0	161117 3 AC008311	AC008311 Drosophi
C 92	16	80.0	163384 9 AC026409	AC026409 Homo sapi

93 16 80.0 163631 9 AC009276 Homo sapi  
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c 95 16 80.0 172266 3 AC092190 Homo sapi  
c 96 16 80.0 173404 10 AC114559 Mus muscu  
c 97 16 80.0 173906 2 AC034171 Homo sapi  
c 98 16 80.0 175099 2 AC109135 Homo sapi  
c 99 16 80.0 175158 2 AC120531 Homo sapi  
c 100 16 80.0 176981 9 AC136634 Homo sapi

ALIGNMENTS

RESULT 1  
BD218489/c 827 bp DNA linear PAT 17-JUL-2003  
LOCUS BD218489  
DEFINITION Diacylglycerol acyl transferase proteins.  
ACCESSION BD218489.1 GI:33028259  
VERSION JP 2002519051-A/30.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 827)  
AUTHORS Lardizabal, K.D., Hawkins, D. and Thompson, G.A.  
TITLE Diacylglycerol acyl transferase proteins  
JOURNAL Patent: JP 2002519051-A 30 02-JUL-2002;  
CALGENE LLC  
OS Homo sapiens (human)  
PN JP 2002519051-A/30  
PD 02-JUL-2002  
PE 30-JUN-1999 JP 2000558114  
PF 02-JUL-1999 US 60/091631, 23-APR-1999 US 60/130829 PI  
KATHRYN DENNIS LARDIZABAL, DEBORAH HAWKINS, GREGORY A THOMPSON PC  
C12N15/09, A01H5/00, A61K45/00, A61P3/04, A61P3/06, A61P3/10 PC  
A61P9/00, A61P35/00,  
PC C07K16/40, C12N5/10, C12N9/10, C12R1.66, C12R1.865, PC  
C12N15/00,  
PC C12N5/00  
CC Diacylglycerol acyl transferase proteins  
FH Key Location/Qualifiers  
FT source 1..827  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 479 GCATTGCCACTCCCATCTT 460

RESULT 2  
BD218493/c 885 bp DNA linear PAT 17-JUL-2003  
LOCUS BD218493  
DEFINITION Diacylglycerol acyl transferase proteins.  
ACCESSION BD218493  
VERSION JP 2002519051-A/34.  
KEYWORDS Mus sp.  
SOURCE Mus sp.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 885)  
AUTHORS Lardizabal, K.D., Hawkins, D. and Thompson, G.A.

TITLE Diacylglycerol acyl transferase proteins  
JOURNAL Patent: JP 2002519051-A 34 02-JUL-2002;  
CALGENE LLC  
COMMENT Mus sp. (murine)  
OS Mus sp.  
PN JP 2002519051-A/34  
PD 02-JUL-2002  
PE 30-JUN-1999 JP 2000558114  
PF 02-JUL-1999 US 60/091631, 23-APR-1999 US 60/130829 PI  
KATHRYN DENNIS LARDIZABAL, DEBORAH HAWKINS, GREGORY A THOMPSON PC  
C12N15/09, A01H5/00, A61K45/00, A61P3/04, A61P3/06, A61P3/10 PC  
A61P9/00, A61P35/00,  
PC C07K16/40, C12N5/10, C12N9/10, C12R1.66, C12R1.865, PC  
C12N15/00,  
PC C12N5/00  
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ORIGIN  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 482 GCATTGCCACTCCCATCTT 463

RESULT 3  
AY675174/c 933 bp mRNA linear MAM 28-JUL-2004  
LOCUS AY675174  
DEFINITION Bos taurus DGAT2 mRNA, partial cds.  
ACCESSION AY675174  
VERSION AY675174.1 GI:50541688  
KEYWORDS Bos taurus (cow)  
SOURCE Bos taurus  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 933)  
AUTHORS Xu, X.R. and Xu, S.Z.  
TITLE Direct Submission  
JOURNAL Submitted (01-JUL-2004) Institute of Animal Science, Academic of  
Agriculture Science of China, Haidian District, Beijing 100094,  
China  
FEATURES  
source Location/Qualifiers  
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/organism="Bos taurus"  
/mol\_type="mRNA"  
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<1..812  
/codon\_start=3  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20

Db 343 GCATTGCCACCTCCATTCTT 324

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RESULT 4  
LOCUS CO723322 1158 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 9256 from Patent WO02068579.  
ACCESSION CO723322  
VERSION CO723322.1 GI:42284179  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of  
humanecons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A, 9256 06-SEP-2002;  
PB Corporation (NY) (US)  
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source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCACCTCCATTCTT 20  
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Db 698 GCATTGCCACCTCCATTCTT 679

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RESULT 5  
AX430068/c 1167 bp DNA linear PAT 21-JUN-2002  
LOCUS AX430068  
DEFINITION . Sequence 2 from Patent WO0208260.  
ACCESSION AX430068  
VERSION AX430068.1 GI:21541216  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 Botstein, D., Brown, P.O., Perou, C., Rose, D. and Seltz, R.  
AUTHORS Bcep-ecg1 protein and related reagents and methods of use thereof  
TITLE Patent: WO 0208260-A 2 31-JAN-2002;  
JOURNAL STANFORD UNIVERSITY (US) ; Applied Genomics, Inc. (US)  
FEATURES  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCACCTCCATTCTT 20  
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Db 698 GCATTGCCACCTCCATTCTT 679

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RESULT 6  
AF384161/c

LOCUS AF384161 1233 bp mRNA linear PRI 11-JAN-2002  
DEFINITION Homo sapiens diacylglycerol acyltransferase 2 mRNA, complete cds.  
ACCESSION AF384161  
KEYWORDS AF384161.2 GI:18129608  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Cases, S., Stone, S.J., Zhou, P., Yen, E., Tow, B., Lardizabal, K.D.,  
Voelker, T. and Farese, R.V., Jr.  
TITLE Cloning of DGAT2, a second mammalian diacylglycerol  
acyltransferase, and related family members  
JOURNAL J. Biol. Chem. 276 (42), 38870-38876 (2001)  
MEDLINE 21486408  
PUBMED 11481335

REFERENCE  
AUTHORS Cases, S., Stone, S., Zhou, P. and Farese, R.V., Jr.  
TITLE Direct Submmission  
JOURNAL Submitted (23-MAY-2001) Gladstone Institutes, 2550 23rd Street, San  
Francisco, CA 94110, USA  
COMMENT On Jan 11, 2002 this sequence version replaced gi:1509952.  
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source Location/Qualifiers  
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/protein\_id="AAK84176.2"  
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HPHGIMGIGAFQNPSTGATEVSKRPGRIPIRYLATLAFPMPLVRYRLMSGICPVR  
DTIDYLSKRGSGNATITIVGGAESLSISPGKRAYTLRRKGVKALRRGALVPI  
YSFGENRVRQVIFEEBSGWRWQKRFQYTGPACTFHGRGLFSSTPWGLVPSKPI  
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Query Match 100.0%; Score 20; DB 9; Length 1233;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCACCTCCATTCTT 20  
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Db 705 GCATTGCCACCTCCATTCTT 686

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RESULT 7  
BD135168/c 1304 bp DNA linear PAT 18-SEP-2002  
LOCUS BD135168  
DEFINITION Human nucleic acid sequence originating in normal mammary tissue.  
ACCESSION BD135168  
VERSION BD135168.1 GI:23230113  
KEYWORDS JP 2002506639-A/15.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Specit, T., Hintzman, B., Shemitt, A., Piariski, C., Duhl, E. and  
Rosenthal, A.  
TITLE Human nucleic acid sequence originating in normal mammary tissue  
JOURNAL Patent: JP 2002506639-A 15 05-MAR-2002  
COMMENT METAGEN GESELSCHAFT FUER GENOME FORSCHUNG MBH  
OS Homo sapiens (human)  
PN JP 2002506639-A/15  
PD 05-MAR-2002

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PF 19-MAR-1999 JP 2000536838
PR 20-MAR-1998 DE 198 13 835.0
PI THOMAS SPEFT, BERND HINZMAN, ARMIN SCHMITT, CHRISTIAN PIRARSKI,
PI EDGAR DURL,
PI ANDRE ROSENTHAL
PC C12N15/09, A61K48/00, A61P35/00, A61P43/00, C07K14/47,
PC C07K16/18,
PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//A61K38/00, PC
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PC C12N5/00, A61K37/02
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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCACTCCCATTCCTT 20
151 GCATTGCCACTCCCATTCCTT 132
Db 151 GCATTGCCACTCCCATTCCTT 132
RESULT 8
LOCUS AX017478 1304 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 21 from Patent WO9947655.
ACCESSION AX017478
VERSION AX017478.1 GI:10042275
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and
Pilarczyk, C.
Human nucleic acid sequences from normal breast tissue
JOURNAL
TITLE Patent: WO 9947655-A 21 23-SEP-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMAN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCACTCCCATTCCTT 20
151 GCATTGCCACTCCCATTCCTT 132
Db 151 GCATTGCCACTCCCATTCCTT 132
RESULT 9
LOCUS AF384160 1330 bp mRNA linear ROD 16-OCT-2001
DEFINITION Mus musculus diacylglycerol acyltransferase 2 mRNA, complete cds.
ACCESSION AF384160
VERSION AF384160.1 GI:15099950
KEYWORDS
FEATURES

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SOURCE
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1330)
Caeses, S., Stone, S.J., Zhou, P., Yen, E., Tow, B., Lardizabal, K.D.,
Voelker, T. and Farese, R.V. Jr.
Cloning of DGAT2, a second mammalian diacylglycerol
acyltransferase, and related family members
J. Biol. Chem. 276 (42), 38870-38876 (2001)
JOURNAL
MEDLINE 21486408
PUBMED 11481335
REFERENCE
2 (bases 1 to 1330)
Caeses, S., Stone, S., Zhou, P. and Farese, R.V. Jr.
Direct Submission
JOURNAL Submitted (23-MAY-2001) Gladstone Institutes, 2550 23rd Street, San
Francisco, CA 94110, USA
FEATURES
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/db_xref="GI:15099951"
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SILSALODIFSVTLNRSKVERKLOLVISFLVAGVACSVILMTCTDCLWLI
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Query Match 100.0%; Score 20; DB 10; Length 1330;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCACTCCCATTCCTT 20
757 GCATTGCCACTCCCATTCCTT 738
Db 757 GCATTGCCACTCCCATTCCTT 738
RESULT 10
LOCUS BTAS19787 1433 bp mRNA linear MAM 06-FEB-2004
DEFINITION Bos taurus mRNA for putative diacylglycerol O-acyltransferase
(DGAT2 gene).
ACCESSION AJ519787
VERSION AJ519787.1 GI:42454646
KEYWORDS DGAT2 gene, diacylglycerol O-acyltransferase 2 protein.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 1433)
Winter, A., van Eckveld, M., Bininda Emonds, O.R.P., Habermann, F.A.
and Fries, R.
Genomic organization of the dgat2/mogat gene family in cattle (bos
taurus) and other mammals
(er) Cytogenet. Genome Res. 102: DOI, 10.1159/000075723 (2003)
JOURNAL
TITLE Direct Submission
JOURNAL Submitted (13-NOV-2002) Lehrstuhl fuer Tierzucht, Technische
Universitaet Muenchen, Alte Akademie 12, Freising-Weihenstephan
85354, GERMANY
FEATURES

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IRPLIATAGFRMPVREYLMGSGICVNRDTIYLLSKGSGAIIIVGAAESL
SSMPGNVTLNRNGEYKALNRGADLVPTYSFENEVYKQVIFEESSWGWOKP
OKYIGFACPIFRGLFSSDPMGLVPSKPIITVVGEPITIPRLRPTQDIDLYHAM
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ORIGIN
Query Match 100.0%; Score 20; DB 4; Length 1433;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCCCATCTT 20
Db 815 GCATTGCCATCCCATCTT 796

RESULT 11
LOCUS AX430070 1543 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 4 from Patent WO0208260.
ACCESSION AX430070
VERSION AX430070.1 GI:21541218
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Bocstein,D., Brown,P.O., Perou,C., Ross,D. and Seitz,R.
TITLE
Bcrp-ecg1 protein and related reagents and methods of use thereof
JOURNAL
PATENT: WO 0208260-A 4 31-JAN-2002;
STANFORD UNIVERSITY (US); Applied Genomics, Inc. (US)
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/db_xref="taxon:33630"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCCCATCTT 20
Db 925 GCATTGCCATCCCATCTT 906

RESULT 12
LOCUS BC015234 1554 bp mRNA linear PRI 30-JUN-2004
DEFINITION Homo sapiens diacylglycerol O-acyltransferase homolog 2 (mouse),
ACCESSION BC015234
VERSION BC015234.1 GI:15929601
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

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REFERENCE
AUTHORS
Strauberg,R.L., Felingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buelow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Dichenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schaefer,T.E., Brownstein,M.J., Udell,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McEwan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Wolley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahney,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
Schererch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1554)
Strauberg,R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (HLN)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.simgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/HLN at: http://image.llnl.gov
Series: IRAC Plate: 22 Row: 9 Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 26024196.
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IRPLIATAGFRMPVREYLMGSGICVNRDTIYLLSKGSGAIIIVGAAESL
SSMPGNVTLNRNGEYKALNRGADLVPTYSFENEVYKQVIFEESSWGWOKP
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
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Db 946 GCATTGCCACTCCCATTTCTT 927

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DEFINITION Sequence 335 from Patent WO0168848.  
ACCESSION AX376268  
VERSION AX376268.1 GI:19170525  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Pan, D., Smith, V., Watanabe, C.K., Wood, W.I. and  
Zhang, Z.  
The secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0168848-A 335 20-SEP-2001;  
Genentech, Inc. (US)

JOURNAL  
TITLE Location/Qualifiers  
FEATURES  
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/mol\_type="unassigned DNA"  
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## ORIGIN

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Db 882 GCATTGCCACTCCCATTTCTT 863

RESULT 14  
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LOCUS AX697223  
DEFINITION Sequence 291 from Patent WO0078961.  
ACCESSION AX697223  
VERSION AX697223.1 GI:29498159  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Eaton, D.L., Gao, W.Q., Pan, D., Botstein, D., Fong, S., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I.,  
Grimaldi, C.J., Hillan, K.J., Pooni, N.F., Roy, M.A. and Watanabe, C.K.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0078961-A 291 28-DEC-2000;  
Genentech Inc. (US)

JOURNAL  
TITLE Location/Qualifiers  
FEATURES

## source

1..1570  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
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QY 1 GCATTGCCACTCCCATTTCTT 20  
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Db 882 GCATTGCCACTCCCATTTCTT 863

RESULT 15  
AY358532/c 1570 bp mRNA linear PRI 03-OCT-2003  
LOCUS AY358532  
DEFINITION Homo sapiens clone DNA71164 DGAT2 (UNQ738) mRNA, complete cds.  
ACCESSION AY358532  
VERSION AY358532.1 GI:37182186  
KEYWORDS FLI CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1570)  
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,  
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,  
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,  
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,  
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,  
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,  
Stinson, J., Vagstad, A., Vanden, R., Watanabe, C., Weiland, D., Woods, K.,  
Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,  
Goddard, A., Wood, W.I. and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a large-scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)

## TITLE

JOURNAL  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 1570)  
AUTHORS Clark, H.F.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

## FEATURES

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## gene

## CDS

## ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 1570;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 GCATTGCCATCCCATCTT 20  
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 882 GCATTGCCATCCCATCTT 863

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 DEFINITION Homo sapiens CDNA FLJ23623 fls, clone ADSE01532.  
 ACCESSION AK074203  
 VERSION AK074203.1 GI:18676740  
 KEYWORDS oligo capping, fls (full insert sequence).  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

**REFERENCE**  
 AUTHORS Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsunura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hiroo,M., Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.  
 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 1735)  
 Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.  
 Direct Submission  
 Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flicdn@nigms.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)  
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).  
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**FEATURES**  
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 LOCUS AB073384 2009 bp mRNA linear PRI 26-AUG-2004  
 DEFINITION Homo sapiens infant liver cDNA, clone:HMFN1045, full insert sequence.  
 ACCESSION AB073384  
 VERSION AB073384.1 GI:51555755  
 KEYWORDS FLI cDNA; oligo capping.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

**REFERENCE**  
 1

**AUTHORS** Yamada,S., Ohira,M., Horie,H., Ando,K., Takayasu,H., Suzuki,Y., Sugano,S., Hirata,T., Goto,T., Matsunaga,T., Hiyaama,E., Hayashi,Y., Ando,H., Saita,S., Kaneko,M., Sasaki,F., Hashizume,K., Ohnuma,N. and Nakagawara,A.  
 Expression profiling and differential screening between hepatoblastomas and the corresponding normal livers: Identification of high expression of the PLK1 oncogene as a poor-prognostic indicator of hepatoblastomas  
 Oncogene 23 (35), 5901-5911 (2004)

**JOURNAL**  
 PUBMED 15221005  
 2 (bases 1 to 2009)  
 Nakagawara,A.  
 Direct Submission  
 Submitted (23-OCT-2001) Akira Nakagawara, Chiba Cancer Center Research Institute, Division of Biochemistry; 666-2, Nisuna-cho, Chuo-ku, Chiba, Chiba 260-8717, Japan (E-mail:akirana@cchiba-ccri.chuo.chiba.jp, Tel:81-43-264-5431(ex.5201), Fax:81-43-262-8680)

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**Qy** 1 GCATTGCCATCCCATCTT 20  
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 DEFINITION Sequence 30334 from Patent WO0160860.  
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 VERSION CQ498467.1 GI:41464103  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
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**REFERENCE**  
 1  
 Schlegel,R., Endege,W.O. and Monahan,J.B.  
 Genes differentially expressed in human prostate cancer and their use  
 Patent: WO 0160860-A 30334 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)  
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**FEATURES**  
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ORIGIN

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QY 1 GCATTGCCACTCCCATCTT 20  
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 LOCUS Mus musculus diacylglycerol O-acyltransferase 2, mRNA (cDNA clone  
 MGC:49088 IMAGE:5125951), complete cds.

ACCESSION BC043447  
 VERSION BC043447.1 GI:27693971  
 KEYWORDS MGC.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Weng, J., Hsieh, F.,  
 Diatchenko, L., Marsina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Caeavanc, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,  
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL 12477932  
 2 (bases 1 to 2263)  
 REFERENCE Strausberg, R.  
 DIRECT SUBMISSION  
 TITLE Submitted (09-JUN-2003) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-9590,  
 USA

REMARK  
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@bcgsc.bc.ca  
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
 Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth  
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,  
 Kim McDonald, Amara Maason, Mike R. Mayo, Josh Moran, Ryan Morin,  
 Teika Olson, Diana Palmquist, Anke Petrescu, Anna Liisa Prabh  
 Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska,  
 Duane Small, Jeff Stott, Miranda Tsai, George Yang, Jacques  
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LMNL at: <http://image.lmnl.gov>

FEATURES  
 source

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ORIGIN

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QY 1 GCATTGCCACTCCCATCTT 20  
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 DEFINITION AL834287  
 ACCESSION AL834287.1 GI:21739870  
 VERSION  
 KEYWORDS  
 SOURCE  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.  
 DIRECT SUBMISSION  
 TITLE Submitted (09-JUN-2002) 1, D-85764 Neuherberg, GERMANY  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ), Email: [s.wiemann@dkfz-heidelberg.de](mailto:s.wiemann@dkfz-heidelberg.de),  
 sequenced by BMFZ (Biomedical Research Center at the Charité,  
 Berlin/Germany) within the cDNA sequencing consortium of the German  
 Genome Project  
 This clone (DKFZp67C1711) is available at the RZPD in Berlin.  
 Please contact the RZPD: [Reisourcenzentrum@neuroherweg6.14059](mailto:Reisourcenzentrum@neuroherweg6.14059)  
 Berlin-Charlottenburg, GERMANY; Email: [clone@rzd.de](mailto:clone@rzd.de) Further  
 information about the clone and the sequencing project is available  
 at <http://mips.gsf.de/proj/cDNA/>.  
 Location/Qualifiers  
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FEATURES  
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Db 836 GCATTGCCACTCCCATCTT 817

RESULT 21
AX281630/c 2398 bp DNA linear PAT 02-NOV-2001
LOCUS Sequence 39 from Patent WO0177389.
ACCESSION AX281630
VERSION AX281630.1 GI:16608881
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Shiffman,D., Somogyi,R., Lawn,R., Selthamer,J.J., Porter,G.J.,
Mikita,T. and Tai,J.
Genes expressed in foam cell differentiation
Patent: WO 0177389-A 39 18-OCT-2001;
Incyte Genomics, Inc. (US)
FEATURES
source
1. 2398
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/notes="Incyte ID No: 474682.2"

ORIGIN
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20

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Db 903 GCATTGCCACTCCCATCTT 884

RESULT 22
AX430071/c 2418 bp DNA linear PAT 21-JUN-2002
LOCUS Sequence 5 from Patent WO0208260.
ACCESSION AX430071
VERSION AX430071.1 GI:21541219
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
Botstein,D., Brown,P.O., Perou,C., Ross,D. and Seltz,R.
Bstip-ecgl protein and related reagents and methods of use thereof
Patent: WO 0208260-A 5 31-JAN-2002;
STANFORD UNIVERSITY (US) ; Applied Genomics, Inc. (US)
FEATURES
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1. 2418
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/notes="Consensus sequence derived from IMAGE clones"

ORIGIN
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RESULT 23
BD181466/c 2439 bp DNA linear PAT 15-MAY-2003
LOCUS A gene of which expression changes in psoriasis and a method for e
xamination directed to said gene.
ACCESSION BD181466
VERSION BD181466.1 GI:30792384
KEYWORDS JP 2002330770-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2439)
Imai,Y., Wakimoto,K., Yamada,E., Chiba,H. and Okubo,K.
A gene of which expression changes in psoriasis and a method for e
xamination directed to said gene
Patent: JP 2002330770-A 14 19-NOV-2002;
TANABE SEIYAKU CO LTD
SOURCE OS Homo sapiens (human)
PN JP 2002330770-A/14
PD 19-NOV-2002
PI 25-MAY-2001 JP 2001156529
PI YUJI IMAI,KOJI WAKIMOTO,ERIKO YAMADA,HIROAKI CHIBA,KOSAKU PI
OKUBO
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
,C12N5/10,C12Q1/68
PC G01N33/53,G01N33/53,G01N33/56,G01N33/56,G01N33/56,G01N33/56
of which expression changes in psoriasis and a method for e
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CC CC
FH Key Location/Qualifiers
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Query Match	100.0%	Score 20	DB 9	Length 2439
Beet Local Similarity	100.0%	Pred. No. 0.14		
Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Query	1	GCATTGCCACTCCCATTTCTT	20	
Db	928	GCATTGCCACTCCCATTTCTT	909	
RESULT 25	AX430069/c	2445 bp	DNA	linear
LOCUS	AX430069	2445 bp	DNA	linear
DEFINITION	Sequence 3 from Patent WO0206260.			
ACCESSION	AX430069			
ORIGIN				
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Db	928	GCATTGCCACTCCCATTTCTT	909	
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CDS	CDS			
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FEATURES	FEATURES			
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KEYWORDS	.	
SOURCE	synthetic construct	
ORGANISM	synthetic construct	
REFERENCE	other sequences; artificial sequences.	
AUTHORS	1	
JOURNAL	Bocstein,D., Brown,P.O., Perou,C., Ross,D. and Seitz,R. BstP-egl protein and related reagents and methods of use thereof Patent: WO 0208260-A 3 31-JAN-2002; STANFORD UNIVERSITY (US) ; Applied Genomics, Inc. (US)	
FEATURES	Location/Qualifiers	
source	1..2445 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Nucleotide sequence of a cDNA that encodes BSTP-BG1"	
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Best Local Similarity	100.0%; Pred. No. 0.14;	
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DEFINITION	Sequence 756 from Patent EP1308459.	
ACCESSION	AX747231	
VERSION	AX747231.1	GI:32131619
KEYWORDS	.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Euharpyota; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1	
JOURNAL	Iscgai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamanoto,J.T., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I.T., Seki,N., Yoshikawa,T., Otsuka,M., Negahari,K. and Masuno,Y. Full-length cDNA sequences Patent: EP 1308459-A 756 07-MAY-2003; Helix Research Institute (JP) ; Research Association for Biotechnology (JP) Location/Qualifiers	
FEATURES	1..2678 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"	
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Db	     2085 GCATTGCCACTCCCATTTCTT 2066	
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DEFINITION	Homo sapiens cDNA FLJ34551 fis, clone HUNG2009413.	
ACCESSION	AK091870	
VERSION	AK091870.1	GI:21750339
KEYWORDS	oligo capping, fls (full insert sequence).	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
1  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Setine, M., Odayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ichii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwamagi, T., Wagaana, M., Shiraori, A., Sudo, H., Hosori, T., Kaku, Y., Kodaira, H., Kondo, H., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Kikawa, M., Yamazaki, M., Niimori, Y., Ieshashi, T., Yamashita, H., Tanikawa, M., Yamazaki, M., Niimori, Y., Matsunawa, H., Ichihara, T., Murakawa, K., Fujimori, K., Tani, H., Kimeta, M., Watanabe, M., Hiraoaka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoda, M., Hottu, T., Kusano, J., Kanehori, K., Takahashi, Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imoe, N., Mueshino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshioka, Y., Matsunawa, H., Ichihara, T., Shichita, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Teshima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Ozaki, K., Hirao, M., Ohnori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Ohtani, R., Kawakami, T., Noguchi, S., Itoh, T., Shiga, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaishi, T., Oyama, M., Hara, H., Watanabe, M., Komatsu, T., Matsushima, Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Maeno, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL  
PUBMED  
14702039

TITLE  
Nat. Genet. 36 (1), 40-45 (2004)

REFERENCE  
AUTHORS  
2  
Taahito, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ichii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Setine, M., Kikuchi, H., Kanda, K., Wagaana, M., Murakami, K., Kanehori, K., Takahashi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Maeno, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
3 (bases 1 to 2678)

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
Isogai, T. and Yamamoto, J. Direct Submission

COMMENT  
Submitted (04-JUL-2002) Takao Isogai, FUJ Project (HRI Team); 2-6-7 Kasuga-Kamatari, Kasarazu, Chiba 292-0812, Japan (E-mail:genomc@hri.co.jp; Tel:01-438-52-3975; Fax:01-438-52-3986)

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DEFINITION	A gene of which expression changes in psoriasis and a method for e								
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ACCESSION	BD181467								
VERSION	BD181467.1	GI:30792385							
KEYWORDS	JP 2002330770-A/15.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
REFERENCE	1 (bases 1 to 2713)								
AUTHORS	Imai,Y., Wakimoto,K., Yamada,E., Chiba,H. and Okubo,K.								
TITLE	A gene of which expression changes in psoriasis and a method for e								
	xamination directed to said gene								
	Patent: JP 2002330770-A 15 19-NOV-2002;								
JOURNAL	TANABE SETYAKU CO LTD								
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	PN JP 2002330770-A/15								
	PD 19-NOV-2002								
	PI 25-MAY-2001 JP 2001156529								
	PI YUJI IMAI,KOJI WAKIMOTO,ERIKO YAMADA,HIROAKI CHIBA,KOSAKU PI								
	OKUBO								
	PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC								
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Best Local Similarity	100.0%;	Pred. No.							

JOURNAL (er) Cytogenet. Genome Res. 102: DOI, 10.1159/000075723 (2003)  
 REFERENCE 2 (bases 1 to 2788)  
 AUTHORS Winter, A.  
 JOURNAL Direct Submission  
 Submitted (13-NOV-2002) Lehrstuhl fuer Tierzucht, Technischen  
 Universitaet Muenchen, Alte Akademie 12, Freising-Weihenstephan  
 85354, GERMANY

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 DEFINITION complete sequences.  
 ACCESSION AP003031  
 VERSION AP003031 GI:17939953  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.,  
 TITLE Homo sapiens genomic DNA  
 JOURNAL Published Only in Database (2000)  
 AUTHORS 2 (bases 1 to 95585)

JOURNAL Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.,  
 TITLE Direct Submission  
 JOURNAL Submitted (08-DEC-2000) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail: hattori@psc.riken.go.jp, URL: http://hgp.psc.riken.go.jp/  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 On Dec 19, 2001 this sequence version replaced gi:14625395.

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#### ORIGIN

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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 7993 GCATTGCCACTCCCATCTT 7974

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 LOCUS AC111120/c Mus musculus chromosome 7 clone RP23-225M4 map 7, \*\*\* SEQUENCING IN  
 DEFINITION PROGRESSES \*\*\*; 8 unordered pieces.

AC111120 AC111120.4 GI:52319138  
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 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus

REFERENCE 1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 AUTHORS Birren, B., Nussbaum, C. and Lander, E.  
 TITLE 1 (bases 1 to 146346)  
 JOURNAL Mus musculus chromosome 7, clone RP23-225M4  
 REFERENCE 2 (bases 1 to 146346)  
 AUTHORS Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,  
 Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,  
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
 Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,  
 Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,  
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 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
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 Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R.,  
 Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,  
 MacDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,  
 McEwan, P., McKernan, K., Meldrum, J., Menue, L., Mhoya, T.,  
 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,  
 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
 Peterson, K., Phunckhang, P., Pierre, N., Pollara, V., Raymond, C.,  
 Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,  
 Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S.,  
 Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodose, J.,  
 Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G.,  
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

REFERENCE 3 (bases 1 to 146346)  
 TITLE Direct Submission  
 JOURNAL Submitted (18-FEB-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 3 (bases 1 to 146346)  
 AUTHORS Birren, B., Nussbaum, C., Lander, E., Abouellail, A., Allen, N.,  
 Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,  
 Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J.,  
 Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B.,  
 Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,  
 Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,  
 Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Halez, N.,

Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, O., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneses, L., Milhova, T., Miengo, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

**TITLE**  
JOURNAL  
Submitted (18-SEP-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Sep 18, 2004 this sequence version replaced gi:5188962.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@broad.mit.edu  
----- Project Information  
Center project name: L22508  
Center clone name: 225\_M\_4

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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 7912: contig of 7912 bp in length  
\* 7913 8012: gap of unknown length  
\* 8013 36022: contig of 28010 bp in length  
\* 36023 36122: gap of unknown length  
\* 36123 49863: contig of 13741 bp in length  
\* 49864 49863: gap of unknown length  
\* 49864 56757: contig of 6794 bp in length  
\* 56758 56857: gap of unknown length  
\* 56858 59875: contig of 3018 bp in length  
\* 59876 59976: gap of unknown length  
\* 59976 80009: contig of 20034 bp in length  
\* 80010 80109: gap of unknown length  
\* 80110 88875: contig of 8766 bp in length  
\* 88876 88976: gap of unknown length  
\* 88976 146346: contig of 57371 bp in length.

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/db\_xref="taxon:10090"  
/chromosome="7"  
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/clone="RP23-225M4"  
/clone\_lib="RP23-225 Female Mouse BAC"

**ORIGIN**  
Query Match 100.0%; Score 20; DB 2; Length 146346;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 GCATTGCCATCTCCATCTTT 20  
|||||  
Db 130951 GCATTGCCATCTCCATCTTT 130932

**RESULT 32**  
AC115850/c  
LOCUS  
DEFINITION  
Mus musculus chromosome 7 clone RP24-252010 map 7, \*\*\* SEQUENCING  
IN PROGRESS \*\*\*, 4 unordered pieces.  
AC115850  
AC115850.7 GI:54111344  
HTG: HTGS PHASE1; HTGS FULLTOP; HTGS\_ACTIVEFIN.  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

**REFERENCE**  
AUTHORS  
JOURNAL  
REFERENCE  
AUTHORS  
Mus musculus chromosome 7, clone RP24-252010  
Unpublished  
2 (bases 1 to 155227)  
Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeRellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C., McCarty, M., McEwan, P., McKernan, K., Meldrum, J., Meneses, L., Milhova, T., Miengo, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strausen, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

**TITLE**  
JOURNAL  
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 155227)  
**REFERENCE**  
AUTHORS  
Birren, B., Nussbaum, C., Lander, E., Abouliell, A., Allen, N., Anderson, M., Anderson, S., Archchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, D., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Darelano, K., Diaz, J. S., Dodge, S., Doolley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneses, L., Milhova, T., Miengo, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

**TITLE**  
JOURNAL  
Submitted (13-OCT-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Oct 13, 2004 this sequence version replaced gi:5188962.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/MIT Center for Genome Research

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Center code: W1BR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@road.mit.edu
-----
Project Information
Center project name: L24674
Center clone name: 252_O_10
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 45393: contig of 45393 bp in length
* 45394 45493: gap of unknown length
* 45494 94478: contig of 48985 bp in length
* 94479 94578: gap of unknown length
* 94579 113577: contig of 18999 bp in length
* 113578 113677: gap of unknown length
* 113678 155227: contig of 41550 bp in length.
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Location/Qualifiers
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/db_xref="taxon:10090"
/chromosome="7"
/map="7"
/clone="RP24-252010"
/clone_11b="RP24 Male Mouse BAC"

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 155227;
Best local Similarity 100.0%; Pred. No. 0.11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20
37818 GCATTGCCACTCCCATCTT 37799

RESULT 33
AC021221 162719 bp DNA linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 11 clone RP11-535A19, WORKING DRAFT
DEFINITION SEQUENCE, 16 unordered pieces.
AC021221
AC021221 GI:7232190
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 162719)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 162719)
Waterston,R.H.
Direct Submission
Submitted (15-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi.7024104.

COMMENT
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Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H NH0535A19
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Summary Statistics
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Sequencing vector: M13, 91%
Sequencing vector: plasmid, 9%
Chemistry: Dye-terminator Big Dye, 9% of reads
Chemistry: Dye-terminator Big Dye, 9% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 151216 bases at least Q40
Consensus quality: 155281 bases at least Q30
Consensus quality: 157953 bases at least Q20
Insert size: 16800; agarose-fp
Insert size: 161219; sum-of-contigs
Quality coverage: 3.91 in Q20 bases; agarose-fp
Quality coverage: 4.11 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1113: contig of 1113 bp in length
* 1114 1213: gap of unknown length
* 1214 3315: contig of 2102 bp in length
* 3316 3415: gap of unknown length
* 3416 5298: contig of 1883 bp in length
* 5299 5398: gap of unknown length
* 5399 8550: contig of 3152 bp in length
* 8551 8650: gap of unknown length
* 8651 12595: contig of 3945 bp in length
* 12596 12695: gap of unknown length
* 12696 17345: contig of 4650 bp in length
* 17346 17445: gap of unknown length
* 17446 21339: contig of 3894 bp in length
* 21340 21439: gap of unknown length
* 21440 26989: contig of 5550 bp in length
* 26990 27089: gap of unknown length
* 27090 34149: contig of 7060 bp in length
* 34150 34249: gap of unknown length
* 34250 47612: contig of 13363 bp in length
* 47613 47712: gap of unknown length
* 47713 59240: contig of 11528 bp in length
* 59241 59340: gap of unknown length
* 59341 74225: contig of 14885 bp in length
* 74226 74325: gap of unknown length
* 74326 89758: contig of 15433 bp in length
* 89759 89858: gap of unknown length
* 89859 108185: contig of 18327 bp in length
* 108186 108285: gap of unknown length
* 108286 132109: contig of 23824 bp in length
* 132110 132209: gap of unknown length
* 132210 162719: contig of 30510 bp in length.
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1214..3315
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3416..5298
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5399..8550
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8651..12595
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Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCATCCCATCTT 20
Db 111632 GCATTGCCATCCCATCTT 111651

RESULT 34
LOCUS AY589091S2/c 721 bp DNA linear NAM 04-MAY-2004
DEFINITION Bos taurus diacylglycerol O-acyltransferase 2 (DGAT2) gene, exons
ACCESSION AY589092
VERSION AY589092.1 GI:46850516
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 721)
XU,X.R., XU,S.Z. and LI,J.Y.
Direct Submission
Submitted (02-APR-2004) Department of Animal Science, Academic of
Agriculture Science of China, Haidian District, Beijing 100094,
China

FEATURES
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Location/Qualifiers
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659..>721
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CATTGCCATCCCATCTT 20
Db 721 CATTGCCATCCCATCTT 703

RESULT 35
LOCUS AE004034 10013 bp DNA linear BCT 04-JUN-2004
DEFINITION Xylella fastidiosa 945c, section 180 of 229 of the complete genome.
ACCESSION AE004034 AE003989
VERSION AE004034.1 GI:9107358
KEYWORDS
SOURCE
ORGANISM
Xylella fastidiosa 945c
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
1 (bases 1 to 10013)
Simpson,A.J., Rainach,F.C., Arruda,P., Abreu,F.A., Acencio,M.,
Alvarenga,R., Alves,L.M., Araya,J.E., Baia,G.S., Baptista,C.S.,
Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Brites,M.R.,
Bueno,M.R., Camargo,A.A., Camargo,L.E., Carraro,D.M., Carreir,H.,
Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C., Costa-Neto,C.M.,
Coutinho,L.L., Cristofani,M., Dias-Neto,E., Docena,C., El-Dorry,H.,
Facincani,A.P., Ferreira,A.J., Ferreira,V.C., Ferro,J.A.,
Fraga,J.S., Franca,S.C., Franco,M.C., Frohme,M., Furlan,L.R.,
Garnier,M., Goldman,G.H., Goldman,M.H., Gomes,S.L., Gruber,A.,
Ho,P.L., Hohnsels,J.D., Junqueira,M.L., Kemper,E.L., Kitejima,J.P.
and Martino,C.L.
The genome sequence of the plant pathogen Xylella fastidiosa. The
Xylella fastidiosa Consortium of the Organization for Nucleotide
Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
JOURNAL
MEDLINE
PUBMED
10910347
2 (bases 1 to 10013)
Simpson,A.J.G., Rainach,F.C., Arruda,P., Abreu,F.A., Acencio,M.,
Alvarenga,R., Alves,L.M.C., Araya,J.E., Baia,G.S., Baptista,C.S.,
Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Brites,M.R.S.,
Bueno,M.R.P., Camargo,A.A., Camargo,L.E.A., Carraro,D.M., Carreir,H.,
Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C., Costa-Neto,E.,
Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J.S.,
Ferreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Franco,M.C.,
Frohme,M., Furlan,L.R., Garnier,M., Goldman,G.H., Goldman,M.H.S.,
Gomes,S.L., Gruber,A., Ho,P.L., Hohnsels,J.D., Junqueira,M.L.,
Kemper,E.L., Kitejima,J.P., Krieger,J.E., Kurmaa,E.B., Laigret,F.,
Lambais,M.R., Leite,L.C.C., Lemos,E.G.M., Lemos,M.V.P., Lopes,S.A.,
Lopes,C.R., Machado,J.A., Machado,M.A., Medeira,A.B.N.,
Medeira,H.M.F., Martino,C.L., Marques,M.V., Martins,E.A.L.,
Martins,E.M.F., Matsukuma,A.Y., Menck,C.F.M., Miracco,E.C.,
Miyaki,C.Y., Monteiro-Vitorello,C.B., Moon,D.H., Nagai,M.A.,
Nascimento,A.L.T.O., Netto,L.E.S., Nhami,J.R., Nobrega,F.G.,
Nunes,L.R., Oliveira,M.A., de Oliveira,M.C., de Oliveira,R.C.,
Palmieri,D.A., Paris,A., Peixoto,B.R., Pereira,G.A.G., Pereira
Jr.,H.A., Pesquero,J.B., Queglio,R.B., Roberto,P.G., Rodrigues,V.,
de M. Rosa,A.J., de Rosa Jr.,V.E., de Sa,R.G., Santelli,R.V.,
Sawaasaki,H.E., da Silva,A.C.R., da Silva,P.R., da Silva,A.M., Silva
Jr.,W.A., da Silveira,J.F., Silvestri,M.L.Z., Siqueira,W.J., de
Souza,A.A., de Souza,A.P., Terezzi,M.F., Truffi,D., Tsai,S.M.,
Tuhakso,M.H., Vallada,H., Van Sluys,M.A., Verjovski-Almeida,S.,
Vettore,A.L., Zago,M.A., Zatz,M., Zedalis,J. and Setubal,J.C.
Direct Submission
Submitted (02-JUN-2000) Organization for Nucleotide Sequencing and
Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas, SP
13083-970, Brazil
Location/Qualifiers
1..10013
FEATURES
source

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  /protein_id="AAF85012.1"
  /db_xref="GI:9107360"
  /translation="MCNEPATSDVALPDLMKAGDGLPEIVQADATLRVLMGYMNS
  QALEVQSRRLVTFYRSKQRLMTKGRSGHVLVAIDADCADDTLIVQAPRPGTC
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  alignment coverage: 99.6 %/subject alignment coverage:
  99.2 %); identified by sequence similarity; putative; ORF
  located using Glimmer/RBSfinder"
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  /translation="MISRLIPCLDVRDGRVYKVKFRDHDVMDGDIVELATRYRDGA
  DFLVFYDIGASPRGRSVDYRWVERVARLIDIPCVAGGIGQETARAVLHAGADKISI
  NSPALRQPLIALABAFGVCVVGIGISIRADQOMRVCNTGDPDKTQALPLRTLD
  MVEARQAGEIVLNCMDSDGRCGYDIAQSARALCOVPLVASGAGMNGHADV
  FKADVQGLASVPHSGAILIPGLKQFLREQQIEVRDY"
  complement (1728..2525)
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  /note="similar to SP|P10371 (percent identity: 44 %/query
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  carboxamide ribotide isomerase"
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  /db_xref="GI:9107362"
  /translation="NMFIVYPALDIRNGAVVRLQGGDYARQTRDDQVLPALAFADS
  GATWHLVDLAKAGGYTLAPLRLQMTKRAQLOVQOTGGSRSDVARIIDAGAAAY
  VIGSLAVESARVIEMLQFGERITVALDRODQGVWRPLVGMTFVAATLDVLA
  QOYAAAGRHLLCTDIARDGMISGNMNVYITLALVPAVOLQVSGARVADVAAK
  MAGCAGIVLGALEGRLLAKRAVGQGSVADPSDPLPGELTEPVC"
  CDS
gene
  /organism="Xylella fastidiosa 9a5c"
  /mol_type="genomic DNA"
  /db_xref="taxon:160492"
  /clone="9a5c"
  70..237
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  similarity; putative; ORF located using Glimmer/RBSfinder"
  /codon_start=1
  /transl_table=11
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  /protein_id="AAF85011.1"
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  bifunctional enzyme"
  /protein_id="AAF85012.1"
  /db_xref="GI:9107360"
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  QALEVQSRRLVTFYRSKQRLMTKGRSGHVLVAIDADCADDTLIVQAPRPGTC
  HIGRTSCPPAAGQFLGALDALVAERERPODSYTTALFEQGVRIAKVGBEVERT
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  /product="cyclase"
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  /db_xref="GI:9107361"
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  DFLVFYDIGASPRGRSVDYRWVERVARLIDIPCVAGGIGQETARAVLHAGADKISI
  NSPALRQPLIALABAFGVCVVGIGISIRADQOMRVCNTGDPDKTQALPLRTLD
  MVEARQAGEIVLNCMDSDGRCGYDIAQSARALCOVPLVASGAGMNGHADV
  FKADVQGLASVPHSGAILIPGLKQFLREQQIEVRDY"
  complement (1728..2525)
  /locus_tag="XF2215"
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  /note="similar to SP|P10371 (percent identity: 44 %/query
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  located using Glimmer/RBSfinder"
  /codon_start=1
  /transl_table=11
  /product="phosphoribosylformimino-5-aminoimidazole
  carboxamide ribotide isomerase"
  /protein_id="AAF85014.1"
  /db_xref="GI:9107362"
  /translation="NMFIVYPALDIRNGAVVRLQGGDYARQTRDDQVLPALAFADS
  GATWHLVDLAKAGGYTLAPLRLQMTKRAQLOVQOTGGSRSDVARIIDAGAAAY
  VIGSLAVESARVIEMLQFGERITVALDRODQGVWRPLVGMTFVAATLDVLA
  QOYAAAGRHLLCTDIARDGMISGNMNVYITLALVPAVOLQVSGARVADVAAK
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  /db_xref="GI:9107363"
  /translation="MTETVALTDAGANIGSVYALORLGVPRPLVCARLEGAAAY
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  VRLPLPASTIRPHGMRLPLPASPLVLEFGASAVFHYAVPLTTAAVACDH
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  complement (3121..4248)
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  located using Glimmer/RBSfinder"
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  /product="imidazoleglycerolphosphate
  dehydratase/histidinol-phosphate phosphatase bifunctional
  enzyme"
  /protein_id="AAF85016.1"
  /db_xref="GI:9107364"
  /translation="MPEPIFIDPRGTLIEEPPQIDAYEKLVLNVGTPALLKTBDA
  GYHVIYTNQDGLSPYPPASBPAPALMLQIFSSGIFRVDLDRSPTDAPLR
  KEGIGLWVALIHQDDIDWARSAMWGDPTLOQPAENININGFOLRTPOFGDWDCGI
  AHTLADAPRRAVVGRTKETTIRVEIDLDGAPARITTGAPFPDMLLEQIAKAGISL
  QISAVGDLIHIDENHIEDTIGLALGOAVRQALGKRGIGRGPDPLPMVSGAAAG
  GFTLPMDETQASAVLDFSGRPYCVFSECTFFRERGDWPTLVHPFRLSLDAGMNLH
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  complement (4245..5342)
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  /locus_tag="XF2218"
  /note="similar to SP|P06986 (percent identity: 42 %/query
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  located using Glimmer/RBSfinder"
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  /transl_table=11
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  /protein_id="AAF85017.1"
  /db_xref="GI:9107365"
  /translation="MNTQTPYVDVYRQELRNAGYSASRVALTGDMLNANESAMP
  NPASHTAKIRFPBPQPKRQMLALYGVPEQLLIGRSDGIDLLVRAVEPCD
  PVLVTPVFGMVAVASQANAVYIQVPLVDDAGFADVAPAITAQTSAKLVFCS
  PSNPVGAIPLOQIETITLQTLAGTALVVDEAGESSDPSVPLARVHLVLRTL
  SKAHLAAVIRIGSVIADAHVAILRQCAPYPTPCVSLAEQGLSAAALQVYRAOVA
  EIRAEERLGAALACLSGVRVYPSQGNFLVAFDDABALQLVAAGVVVRQRAAP
  QLDHALRLTYGTGEONTRLIAYLRDQAVPA"
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gene
  Query Match 85.0%; Score 17; DB 1; Length 10013;
  Best Local Similarity 100.0%; Pred. No. 8.7;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  4 TTGGCACTCCCAITCTT 20
  Oy
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Db 7177 TTGCCACTCCATCTT 7193

RESULT 36  
AL954659/c 43593 bp DNA linear PRI 02-DEC-2002  
LOCUS Human DNA sequence from clone RP11-142D11 on chromosome X, complete  
DEFINITION sequence.  
AL954659  
ACCESSION AL954659.4 GI:26185670  
VERSION HTG.  
KEYWORDS Homo sapiens (human)  
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
ORGANISM  
REFERENCE  
AUTHORS Wray, P.  
TITLE Direct Submission  
JOURNAL Submitted (30-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
On Dec 6, 2002 this sequence version replaced gi:25809658.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: humquerry@sanger.ac.uk

-----  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX>

RP11-142D11 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pBAC3.6

FEATURES  
source location/Qualifiers

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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="X"  
/clone="RP11-142D11"  
/clone\_lib="RPCI-11.1"

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 43593;  
Best Local Similarity 100.0%; Pred. No. 7.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0y 2 CATTGCCACTCCCATTC 18  
|||||  
Db 29329 CATTGCCACTCCCATTC 29313

RESULT 37  
AC100360  
LOCUS AC100360  
DEFINITION Mus musculus clone RP23-128F24, LOW-PASS SEQUENCE SAMPLING.  
AC100360  
VERSION AC100360.1 GI:17047726  
KEYWORDS HTG; HTGS PHASED.  
SOURCE Mus musculus (house mouse)  
ORGANISM  
REFERENCE  
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
TITLE 1 (bases 1 to 69294)  
JOURNAL Mus musculus, clone RP23-128F24  
REFERENCE  
AUTHORS 2 (bases 1 to 69294)  
JOURNAL Unpublished  
REFERENCE  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Baatien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choquel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dehtrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S., Glinde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karates, A., Kellis, C., Larocque, K., Lamazeres, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Menus, L., Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retra, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strausman, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zaitoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
JOURNAL Direct Submission  
COMMENT Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: W18R  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L15164  
Center clone name: 128\_F\_24

-----  
\* NOTE: This record contains 67 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 946: contig of 946 bp in length  
\* 947 1046: gap of 100 bp  
\* 1047 2020: contig of 974 bp in length  
\* 2021 2120: gap of 100 bp  
\* 2121 3095: contig of 975 bp in length  
\* 3096 3195: gap of 100 bp  
\* 3196 4186: contig of 991 bp in length

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* 4187 4286: gap of 100 bp
* 4287 5159: contig of 873 bp in length
* 5160 5259: gap of 100 bp
* 5260 6149: contig of 890 bp in length
* 6150 6249: gap of 100 bp
* 6250 7179: contig of 930 bp in length
* 7180 7279: gap of 100 bp
* 7280 8280: contig of 1001 bp in length
* 8281 8380: gap of 100 bp
* 8381 9379: contig of 999 bp in length
* 9380 9479: gap of 100 bp
* 9480 10468: contig of 989 bp in length
* 10469 10568: gap of 100 bp
* 10569 11550: contig of 982 bp in length
* 11551 11650: gap of 100 bp
* 11651 12588: contig of 938 bp in length
* 12589 12688: gap of 100 bp
* 12689 13630: contig of 942 bp in length
* 13631 13730: gap of 100 bp
* 13731 14568: contig of 838 bp in length
* 14569 14668: gap of 100 bp
* 14669 15636: contig of 968 bp in length
* 15637 15736: gap of 100 bp
* 15737 16706: contig of 970 bp in length
* 16707 16806: gap of 100 bp
* 16807 17719: contig of 913 bp in length
* 17720 17819: gap of 100 bp
* 17820 18737: contig of 918 bp in length
* 18738 18837: gap of 100 bp
* 18838 19769: contig of 932 bp in length
* 19770 19869: gap of 100 bp
* 19870 20863: contig of 994 bp in length
* 20864 20963: gap of 100 bp
* 20964 21918: contig of 955 bp in length
* 21919 22018: gap of 100 bp
* 22019 22958: contig of 940 bp in length
* 22959 23058: gap of 100 bp
* 23059 23918: contig of 860 bp in length
* 23919 24018: gap of 100 bp
* 24019 24974: contig of 956 bp in length
* 24975 25074: gap of 100 bp
* 25075 26101: contig of 1027 bp in length
* 26102 26201: gap of 100 bp
* 26202 26944: contig of 743 bp in length
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* 27045 27779: contig of 735 bp in length
* 27780 27879: gap of 100 bp
* 27880 28860: contig of 981 bp in length
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* 28961 29882: contig of 922 bp in length
* 29883 29982: gap of 100 bp
* 29983 30957: contig of 975 bp in length
* 30958 31057: gap of 100 bp
* 31058 32006: contig of 949 bp in length
* 32007 32106: gap of 100 bp
* 32107 33030: contig of 924 bp in length
* 33031 33130: gap of 100 bp
* 33131 34113: contig of 983 bp in length
* 34114 34213: gap of 100 bp
* 34214 35121: contig of 908 bp in length
* 35122 35221: gap of 100 bp
* 35222 36181: contig of 960 bp in length
* 36182 36281: gap of 100 bp
* 36282 36968: contig of 687 bp in length
* 36969 37068: gap of 100 bp
* 37069 37989: contig of 921 bp in length
* 37990 38089: gap of 100 bp
* 38090 38998: contig of 909 bp in length
* 38999 39098: gap of 100 bp
* 39099 40029: contig of 931 bp in length
* 40030 40129: gap of 100 bp
* 40130 41007: contig of 878 bp in length
* 41008 41107: gap of 100 bp

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* 41108 42090: contig of 993 bp in length
* 42091 42190: gap of 100 bp
* 42191 43100: contig of 910 bp in length
* 43101 43200: gap of 100 bp
* 43201 44181: contig of 981 bp in length
* 44182 44281: gap of 100 bp
* 44282 45318: contig of 1037 bp in length
* 45319 45418: gap of 100 bp
* 45419 46357: contig of 939 bp in length
* 46358 46457: gap of 100 bp
* 46458 47408: contig of 951 bp in length
* 47409 48412: contig of 904 bp in length
* 48413 48512: gap of 100 bp
* 48513 49448: contig of 936 bp in length
* 49449 49548: gap of 100 bp
* 49549 50533: contig of 985 bp in length
* 50534 50633: gap of 100 bp
* 50634 51583: contig of 950 bp in length
* 51584 51683: gap of 100 bp
* 51684 52692: contig of 1009 bp in length
* 52693 52792: gap of 100 bp
* 52793 53730: contig of 938 bp in length
* 53731 53830: gap of 100 bp
* 53831 54735: contig of 905 bp in length
* 54736 54835: gap of 100 bp
* 54836 55763: contig of 928 bp in length
* 55764 55863: gap of 100 bp
* 55864 56842: contig of 979 bp in length
* 56843 56942: gap of 100 bp
* 56943 57873: contig of 931 bp in length
* 57874 57973: gap of 100 bp
* 57974 58882: contig of 909 bp in length
* 58883 58982: gap of 100 bp
* 58983 59996: contig of 1014 bp in length
* 59997 60096: gap of 100 bp
* 60097 61082: contig of 986 bp in length
* 61083 61182: gap of 100 bp
* 61183 62100: contig of 918 bp in length
* 62101 62200: gap of 100 bp
* 62201 62916: contig of 716 bp in length
* 62917 63016: gap of 100 bp
* 63017 63950: contig of 934 bp in length
* 63951 64050: gap of 100 bp
* 64051 64958: contig of 908 bp in length
* 64959 65058: gap of 100 bp
* 65059 66060: contig of 1002 bp in length
* 66061 66160: gap of 100 bp
* 66161 67113: contig of 953 bp in length
* 67114 67213: gap of 100 bp
* 67214 68204: contig of 991 bp in length
* 68205 68304: gap of 100 bp
* 68305 69294: contig of 990 bp in length.

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FEATURES
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            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"

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Query Match      85.0%; Score 17; DB 2; Length 69294;
Beet Local Similarity 100.0%; Pred. No. 7.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GCATTGCCACTCCATT 17
db      37682 GCATTGCCACTCCATT 37698

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```

RESULT 38
AL365359/c      98637 bp      DNA      linear      HTG 10-JUL-2001
LOCUS          Homo sapiens chromosome 1 clone RFS-102811, 7 unordered pieces.
DEFINITION
ACCESSION      AL365359

```

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VERSION      AL365359.7 GI:11322090
KEYWORDS     HTG; HTGS PHASE1; HTGS_CANCELED.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1
AUTHORS      McLay, K.
TITLE        Direct Submision
JOURNAL      Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
              CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
              requests: clonerequests@sanger.ac.uk
              On Nov 23, 2000 this sequence version replaced gi.9926733.
COMMENT      ----- Genome Center
              Center: Sanger Centre
              Center code: SC
              Web site: http://www.sanger.ac.uk
              Contact: humquery@sanger.ac.uk
              ----- Project Information
              Center project name: dj102811
              ----- Summary Statistics
              Assembly program: XGAP4; version 4.5
              Sequencing vector: plasmid; L08752; 100% of reads
              Chemistry: Dye-terminator ET-amersham; 16% of reads
              Dye-terminator Big Dye; 83% of reads
              Consensus quality: 95773 bases at least Q40
              Consensus quality: 96880 bases at least Q30
              Consensus quality: 97481 bases at least Q20
              Insert size: 98037; sum-of-ctnigs
              Insert size: 94436; 8.5% error; agarose-fp
              Quality coverage: 6.23x in Q20 bases; sum-of-ctnigs
              Quality coverage: 8.33x in Q20 bases; agarose-fp
              -----
              * NOTE: This is a 'working draft' sequence. It currently
              * consists of 7 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              *
              1 6481: contig of 6481 bp in length
              * 6482 6581: gap of 100 bp
              * 6582 9621: contig of 3040 bp in length
              * 9622 9721: gap of 100 bp
              * 9722 12293: contig of 2572 bp in length
              * 12294 12393: gap of 100 bp
              * 12394 47167: contig of 34774 bp in length
              * 47168 47267: gap of 100 bp
              * 47268 51968: contig of 4601 bp in length
              * 51969 66326: gap of 100 bp
              * 66326 98637: contig of 14357 bp in length
              * 98637 98637: gap of 100 bp
              * 98637 98637: contig of 32212 bp in length.
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                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
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                  /clone_lib="RPCI-5"
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                    misc_feature 6582..9621
                      /note="Assembly_fragments:01036"
                      misc_feature 9722..12293
                        /note="Assembly_fragments:01668"
                        misc_feature 12394..47167
                          /note="Assembly_fragments:01209
                          fragment_chain:1"

```

```

misc_feature 47268..51868
  /note="Assembly_fragments:01171
  fragment_chain:1"
misc_feature 51969..66325
  /note="Assembly_fragments:00109
  fragment_chain:1"
misc_feature 66426..98637
  /note="Assembly_fragments:00843
  fragment_chain:1
  clone_end:T7
  vector_side:right"

ORIGIN
Query Match      85.0%; Score 17; DB 2; Length 98637;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATTGCCATCTCCATTTC 18
        |||||
Db       17355 CATTGCCATCTCCATTTC 17339

RESULT 39
HSDJ96108      104695 bp DNA linear PRI 17-APR-2001
LOCUS          Human DNA sequence from clone RPS-96108 on chromosome X Contains
DEFINITION     STSs and GSSs, complete sequence.
ACCESSION      AL121879
VERSION        AL121879.14 GI:6635883
KEYWORDS       HTG.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 104695)
              1..104695
              Direct Submission
              Submitted (17-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
              CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
              requests: clonerequests@sanger.ac.uk
              On Dec 26, 1999 this sequence version replaced gi:6630795.
              During sequence assembly data is compared from overlapping clones.
              Where differences are found these are annotated as variations
              together with a note of the overlapping clone name. Note that the
              variation annotation may not be found in the sequence submission
              only a small overlap as described above.
              The following abbreviations are used to associate primary accession
              numbers given in the feature table with their source databases:
              Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
              on the WORMPEP database can be found at
              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is
              the entire insert of clone RPS-96108 This sequence was generated
              from part of bacterial clone contigs of human chromosome X,
              constructed by the Sanger Centre Chromosome X Mapping Group.
              Further information can be found at
              http://www.sanger.ac.uk/HGP/Chrx
              This sequence was finished as follows unless otherwise noted: all
              regions were either double-stranded or sequenced with an alternate
              chemistry or covered by high quality data (i.e., phred quality >=
              30); an attempt was made to resolve all sequencing problems, such
              as compressions and repeats; all regions were covered by at least
              one plasmid subclone or more than one M13 subclone; and the
              assembly was confirmed by restriction digest. RPS-96108 is from the
              library RPCI-5 constructed by the group of Pieter de Jong. For
              further details see
              http://www.chori.org/bacpac/home.htm
              VECTOR: pCYPAC2
              Location/Qualifiers
                source          1..104695
                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"

```

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/chromosome="X"
/clone="RP5-96108"
/clone_1lb="RPCT-5"
1..272
repeat_region /note="Charlie3 repeat: matches 1..272 of consensus"
repeat_region 304..903 /note="LIR12 repeat: matches 1..541 of consensus"
repeat_region 924..3841 /note="HERV9 repeat: matches 58..2972 of consensus"
repeat_region 3841..7462 /note="HERV9 repeat: matches 4756..8399 of consensus"
repeat_region 7492..8427 /note="LIR12 repeat: matches 323..2438 of consensus"
misc_feature /note="match: STS: Em:LI5215"
9370..9485
repeat_region /note="L2 repeat: matches 2629..2748 of consensus"
9505..9560
repeat_region /note="MIR repeat: matches 70..129 of consensus"
9628..11133
repeat_region /note="LIP repeat: matches 1..1508 of consensus"
1132..14428
repeat_region /note="LIPB4 repeat: matches 2812..6142 of consensus"
14439..14652
repeat_region /note="MIR repeat: matches 20..213 of consensus"
15555..15616
repeat_region /note="L2 repeat: matches 2264..2311 of consensus"
15617..15915
repeat_region /note="AluY repeat: matches 5..302 of consensus"
15916..15985
repeat_region /note="L2 repeat: matches 2190..2264 of consensus"
16270..16714
misc_feature /note="match: STS: Em:HSC76C4"
16600..16867
repeat_region /note="LIMB2 repeat: matches 5888..6155 of consensus"
17004..17145
repeat_region /note="L2 repeat: matches 2553..2701 of consensus"
18344..18576
repeat_region /note="MIR repeat: matches 20..252 of consensus"
19188..19654
repeat_region /note="LIPB3 repeat: matches 5689..6148 of consensus"
19655..19748
repeat_region /note="LIMB2 repeat: matches 6213..6308 of consensus"
19749..19825
repeat_region /note="LIPB3 repeat: matches 5612..5689 of consensus"
20297..20727
repeat_region /note="LIMB3 repeat: matches 5157..5580 of consensus"
20728..21249
repeat_region /note="LIMB3 repeat: matches 5648..6178 of consensus"
21250..21803
repeat_region /note="LIMB3 repeat: matches 5580..6163 of consensus"
complement(23018..23146)
misc_feature /note="match: STS: Em:LI1074"
23979..24205
repeat_region /note="MIR repeat: matches 15..235 of consensus"
25470..25699
repeat_region /note="MER4C repeat: matches 2..236 of consensus"
25769..26063
repeat_region /note="L2 repeat: matches 2367..2669 of consensus"
26092..26573
repeat_region /note="L2 repeat: matches 916..1497 of consensus"
26574..27190
repeat_region /note="LIPB5 repeat: matches 5524..6141 of consensus"
27191..27420
repeat_region /note="L2 repeat: matches 1407..1634 of consensus"
27863..27961
repeat_region /note="LIMB6 repeat: matches 6202..6300 of consensus"
28341..28439
repeat_region /note="MIR repeat: matches 97..202 of consensus"
28880..28937
repeat_region /note="29 copies 2 mer ta 72% conserved"
29100..29360
repeat_region /note="L2 repeat: matches 2406..2648 of consensus"
```

---

```
repeat_region 29912..30599
misc_feature /note="L2 repeat: matches 2003..2710 of consensus"
31474..31981
misc_feature /note="match: GSS: Em:AQ411673"
31501..31774
repeat_region /note="match: GSS: Em:AQ570877"
31941..32122
repeat_region /note="MIR repeat: matches 23..205 of consensus"
32136..32165
repeat_region /note="LIMB9 repeat: matches 6274..6303 of consensus"
32769..32949
repeat_region /note="MIR repeat: matches 20..203 of consensus"
36212..36427
repeat_region /note="MIR repeat: matches 2..231 of consensus"
36925..37076
repeat_region /note="Charlie4 repeat: matches 1801..1955 of consensus"
37146..37333
repeat_region /note="Charlie4 repeat: matches 1..216 of consensus"
37724..38038
repeat_region /note="AluSg repeat: matches 1..310 of consensus"
38225..38346
repeat_region /note="L2 repeat: matches 2371..2491 of consensus"
39416..39653
repeat_region /note="MIR repeat: matches 2..241 of consensus"
40301..40477
repeat_region /note="LIMB3 repeat: matches 6100..6275 of consensus"
40503..40542
repeat_region /note="20 copies 2 mer ta 90% conserved"
40543..40872
repeat_region /note="165 copies 2 mer at 76% conserved"
40893..41008
repeat_region /note="58 copies 2 mer ta 82% conserved"
40994
misc_feature /note="Random repeat. Forced join. gap sized to be 16ss
chan 100 bases from restriction digest data and a spanning
PUC clone."
41535..42210
repeat_region /note="LIMB2 repeat: matches 5502..6164 of consensus"
complement(42043..42740)
misc_feature /note="match: GSS: Em:AQ488567"
42258..42546
repeat_region /note="LIR39 repeat: matches 410..360 of consensus"
complement(42377..42743)
repeat_region /note="match: GSS: Em:AQ169848"
42593..42850
misc_feature /note="MER49 repeat: matches 1..294 of consensus"
42763..43219
repeat_region /note="match: GSS: Em:AQ013777"
42900..42993
repeat_region /note="LIR29 repeat: matches 3..99 of consensus"
43421..43472
repeat_region /note="MER39B repeat: matches 496..547 of consensus"
43554..43822
repeat_region /note="LIMB2 repeat: matches 5219..5481 of consensus"
43875..44159
repeat_region /note="LIPB8 repeat: matches 5589..5874 of consensus"
44198..44561
repeat_region /note="LIM4 repeat: matches 246..1697 of consensus"
45911..46342
repeat_region /note="MER41C repeat: matches 1..508 of consensus"
46343..46406
repeat_region /note="MER41-internal repeat: matches 80..142 of
consensus"
46423..46757
misc_feature /note="match: GSS: Em:AQ099828"
46664..47242
repeat_region /note="HERVB repeat: matches 3388..3967 of consensus"
complement(47170..47402)
misc_feature /note="match: GSS: Em:AQ041904"
47473..48633
repeat_region /note="HERV9 repeat: matches 4694..5853 of consensus"
48403..48866
repeat_region /note="match: GSS: Em:AQ143235"
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```

misc_feature      8882..12361
                  /note="assembly_fragment"
misc_feature      12462..20412
                  /note="assembly_fragment"
misc_feature      20513..28499
                  /note="assembly_fragment"
misc_feature      28600..37268
                  /note="assembly_fragment"
misc_feature      37369..47539
                  /note="assembly_fragment"
                  clone_end:SP6
                  vector_side:left"
misc_feature      47640..61172
                  /note="assembly_fragment"
misc_feature      61273..77119
                  /note="assembly_fragment"
misc_feature      77220..103392
                  /note="assembly_fragment"
                  clone_end:T7
                  vector_side:right"
misc_feature      103493..143454
                  /note="assembly_fragment"

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## ORIGIN

```

Query Match      85.0%; Score 17; DB 2; Length 143454;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 CATTGCCACTCCCATTC 18
        |||||
Db      3978 CATTGCCACTCCCATTC 3994

```

```

RESULT 42
AC027556      156149 bp      DNA      linear      HTG 04-OCT-2000
LOCUS      Homo sapiens chromosome 17 clone RP11-81013 map 17, WORKING DRAFT
DEFINITION      AC027556
SEQUENCE      23 unordered pieces.
AC027556
AC027556.2 GI:10567975
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 156149)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Baerlein,V., Beda,F.,
Boguslavsky,L., Boucklingalter,B., Brown,A., Burkett,G.,
Bogliardo,A., Caele,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Glend,S., Goyette,M., Graham,L.,
Grand-pierre,N., Grant,G., Hages,B., Heatford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,J., Karatae,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehocsky,J.,
Levine,R., Liu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPherson,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessier,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

```

TITLE  
JOURNAL  
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome

## COMMENT

```

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 4, 2000 this sequence version replaced GI:7342301.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submission@genome.wi.mit.edu
----- Project Information
Center project name: B8949
Center clone name: B1_O13
----- Summary Statistics
Sequencing vector: M13; M77815; 94% of reads
Sequencing vector: Plasmid; n/a; 6% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 144286 bases at least Q40
Consensus quality: 150098 bases at least Q20
Consensus quality: 152440 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 153949; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.3 in Q20 bas.
NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
4015 4014: contig of 4014 bp in length
4115 4114: gap of 100 bp
5625 5625: contig of 1511 bp in length
5626 5725: gap of 100 bp
5726 6824: contig of 1099 bp in length
6825 6925 6824: gap of 100 bp
6925 8353: contig of 1429 bp in length
8354 8453: gap of 100 bp
8454 9642: contig of 1189 bp in length
9643 9742: gap of 100 bp
9743 11659: contig of 1917 bp in length
11660 11759: gap of 100 bp
11760 13651: contig of 1892 bp in length
13652 13751: gap of 100 bp
13752 16812: contig of 3061 bp in length
16813 16912: gap of 100 bp
16912 19304: contig of 2392 bp in length
19305 19404: gap of 100 bp
19405 21925: contig of 2521 bp in length
21926 22025: gap of 100 bp
22026 24279: contig of 2254 bp in length
24280 24319: gap of 100 bp
24380 28256: contig of 3877 bp in length
28257 28356: gap of 100 bp
28357 33672: contig of 5316 bp in length
33673 33772: gap of 100 bp
33772 37991: contig of 4219 bp in length
37992 38091: gap of 100 bp
38092 44086: contig of 5995 bp in length
44087 44186: gap of 100 bp
44187 50586: contig of 6400 bp in length
50587 50686: gap of 100 bp
50687 78161: contig of 27475 bp in length
78162 78261: gap of 100 bp
78262 84913: contig of 6632 bp in length
84914 85013: gap of 100 bp
85014 97976: contig of 12663 bp in length
97977 98076: gap of 100 bp
98077 110971: contig of 12855 bp in length
110972 110971: gap of 100 bp

```

FEATURES	
*	111072 126745: config of 15674 bp in length
*	126746 126845: gap of 100 bp
*	126846 145802: config of 18557 bp in length
*	145803 145802: gap of 100 bp
*	145903 156149: config of 10247 bp in length
	Location/Qualifiers

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source
1. .156149
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="RP11-81013"
/clone_lib="RPC1-11 Human Male BAC"
1. .4014
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
4115. .5625
/note="assembly_fragment"
5726. .6824
/note="assembly_fragment"
6925. .8353
/note="assembly_fragment"
8454. .9642
/note="assembly_fragment"
9743. .11659
/note="assembly_fragment"
11760. .13651
/note="assembly_fragment"
13752. .16812
/note="assembly_fragment"
15913. .19304
/note="assembly_fragment"
19405. .21925
/note="assembly_fragment"
22026. .24279
/note="assembly_fragment"
24380. .28255
/note="assembly_fragment"
28357. .33672
/note="assembly_fragment"
33773. .37991
/note="assembly_fragment"
38092. .44086
/note="assembly_fragment"
44187. .50586
/note="assembly_fragment"
50687. .78161
/note="assembly_fragment"
78262. .84913
/note="assembly_fragment"
85014. .97976
/note="assembly_fragment"
98077. .110971
/note="assembly_fragment"
111072. .126745
/note="assembly_fragment"
126846. .145802
/note="assembly_fragment"
145903. .156149
/note="assembly_fragment"
clone_end:17
vector_side:right"

```

Query Match	Score 17:	DB 2:	Length 156149:
Best Local Similarity	100.0%	Pred. No. 7.1:	
Matches 17:	Conservative 0:	Mismatches 0:	Indels 0:
			Gaps 0:
QY	2	CATTGCCACTCCCATTC	18
Db	30936	CATTGCCACTCCCATTC	30952

RESULT 43	
AL928688	
LOCUS	
DEFINITION	AL928688 165910 bp DNA linear PRI 27-SEP-2002
ACCESSION	Human DNA sequence from clone RP11-77N10 on chromosome 10, complete sequence.
VERSION	AL928688
KEYWORDS	AL928688.3 GI:23380957
SOURCE	HTG.
ORGANISM	Homo sapiens (human)
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 165910)
AUTHORS	Clark,S.
TITLE	Direct Submission
JOURNAL	Submitted (27-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humbry@sanger.ac.uk
COMMENT	Clone requests: clonerequest@sanger.ac.uk On Sep 30, 2002 this sequence version replaced gi:23337954.

----- Genome Centre  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk)  
-----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; SW; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr10>

Rpl1-77N10 is from the library RPCI-11.1 constructed by the group of Rister de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.

```

FEATURES
source      location/Qualifiers
1..165910  /organism="Homo sapiens"
           /mol_type="genomic DNA"
           /db_xref="taxon:9606"
           /chromosome="10"
           /clone="RP11-77N10"
           /clone_1b="RPC1-11.1"

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Query Match Score 17; DB 9; Length 165910;  
Best Local Similarity 100.0%; Prod. No. 7.1;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 CATTGCCACCTCCATTC 18  
|||||  
Db 124789 CATTGCCACCTCCATTC 124805

## RESULT 44



AL935036 166004 bp DNA linear PRI 07-NOV-2002  
 LOCUS Human DNA sequence from clone RP11-257E20 on chromosome 10,  
 DEFINITION complete sequence.  
 ACCESSION AL935036  
 VERSION AL935036 GI:24474499  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Howden, P.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Nov 1, 2002 this sequence version replaced gi:24366850.  
 COMMENT  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: humquerry@sanger.ac.uk

-----  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em., EMBL; Sw.,  
 SWISSPROT; Tr., TrEMBL; Wp., WormPeP; information on the WormPeP  
 database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 10, constructed by the Sanger Centre Chromosome 10  
 Mapping Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr10>  
 RP11-257E20 is from the library RPCT-11.1 constructed by the group  
 of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBAC3.6

FEATURES  
 source  
 1..166004  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="10"  
 /clone="RP11-257E20"  
 /clone\_1ib="RPCT-11.1"

ORIGIN  
 Query Match 85.0%; Score 17; DB 9; Length 166004;  
 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATTGCCACTCCCATTC 18  
 |||||  
 Db 55282 CATTGCCACTCCCATTC 55298

RESULT 45  
 AL161734 167099 bp DNA linear PRI 10-MAR-2003  
 LOCUS Human DNA sequence from clone RP11-33M22 on chromosome 1q25.2-31.2,  
 DEFINITION

complete sequence.  
 AL161734  
 VERSION AL161734.12 GI:28933321  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Harrison, E.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Mar 12, 2003 this sequence version replaced gi:1590620.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPeP; information  
 on the WormPeP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping  
 Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr1>  
 RP11-33M22 is from the library RPCT-11.1 constructed by the group  
 of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBAC3.6

----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: humquerry@sanger.ac.uk

-----  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest, except on the rare  
 occasion of the clone being a YAC.

FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="1"  
 /map="q25.2-31.2"  
 /clone="RP11-33M22"  
 /clone\_1ib="RPCT-11.1"

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATTGCCACTCCCATTC 18  
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 Db 69217 CATTGCCACTCCCATTC 69233

Search completed: August 5, 2005, 01:26:41  
 Job time : 1833 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 00:40:17 ; Search time 615 Seconds  
(without alignments)  
210.807 Million cell updates/sec

Title: US-10-643-801A-35  
Perfect score: 20  
Sequence: 1 gcatgcctaccctccctc 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7297361 seqs, 3241162794 residues

Word size : 8

Total number of hits satisfying chosen parameters: 910364

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

Published Applications NA:\*

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- 21: /cgn2\_6/ptodata/1/pubpna/US10J\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	20	100.0	827	14	US-10-121-857-56
5	20	100.0	827	15	US-10-208-018-56
6	20	100.0	885	14	US-10-121-857-60
7	20	100.0	885	15	US-10-208-018-60

8	20	100.0	1030	18	US-10-307-817-539	Sequence 539, App
9	20	100.0	1077	18	US-10-307-817-538	Sequence 538, App
10	20	100.0	1167	9	US-09-794-715A-3	Sequence 3, Appl1
11	20	100.0	1167	15	US-10-278-733-8	Sequence 8, Appl1
12	20	100.0	1167	15	US-10-208-018-97	Sequence 97, Appl
13	20	100.0	1167	15	US-10-208-018-111	Sequence 111, App
14	20	100.0	1167	15	US-10-208-018-126	Sequence 126, App
15	20	100.0	1167	15	US-10-046-924-3	Sequence 3, Appl1
16	20	100.0	1167	17	US-10-286-581-3	Sequence 3, Appl1
17	20	100.0	1167	16	US-10-446-441-3	Sequence 3, Appl1
18	20	100.0	1167	21	US-10-945-738-3	Sequence 3, Appl1
19	20	100.0	1172	18	US-10-307-817-103	Sequence 103, App
20	20	100.0	1189	18	US-10-307-817-101	Sequence 101, App
21	20	100.0	1189	18	US-10-307-817-107	Sequence 107, App
22	20	100.0	1191	18	US-10-307-817-93	Sequence 93, Appl
23	20	100.0	1191	18	US-10-307-817-97	Sequence 97, Appl
24	20	100.0	1198	18	US-10-307-817-105	Sequence 105, App
25	20	100.0	1207	18	US-10-307-817-99	Sequence 99, Appl
26	20	100.0	1230	18	US-10-307-817-95	Sequence 95, Appl
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33	20	100.0	1233	15	US-10-046-924-18	Sequence 18, Appl
34	20	100.0	1233	16	US-10-286-581-18	Sequence 18, Appl
35	20	100.0	1233	21	US-10-945-738-18	Sequence 18, Appl
36	20	100.0	1510	17	US-10-172-118-2665	Sequence 2665, App
37	20	100.0	1510	18	US-10-342-887-2665	Sequence 2665, App
38	20	100.0	1570	13	US-09-946-374-291	Sequence 291, App
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c 89 20 100.0 1570 14 US-10-176-978-335 Sequence 335, App
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## ALIGNMENTS

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US-10-643-801-35
; Sequence 35, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-801-35
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; Sequence 157, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-643-801-157
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Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 GCATTGCCACTCCCATTTCTT 1
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US-10-116-712-436/c
; Sequence 436, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-712-436
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Db 269 GCATTGCCACTCCCATTTCTT 250
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RESULT 4
US-10-121-857-56/c
; Sequence 56, Application US/10121857
; Publication No. US20030028923A1
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.143
; CURRENT APPLICATION NUMBER: US/10/121,857
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 827
; TYPE: DNA
; ORGANISM: Human
US-10-121-857-56
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Db 479 GCATTGCCACTCCCATTTCTT 460
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RESULT 5  
US-10-208-018-56/c  
; Sequence 56, Application US/10208018  
; Publication No. US20030115632A1  
; GENERAL INFORMATION:  
; APPLICANT: Lardizabal, Kathryn D  
; APPLICANT: Hawkins, Deborah J  
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins  
; FILE REFERENCE: 16515.155  
; CURRENT APPLICATION NUMBER: US/10/208,018  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US 10/121,857  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 09/345,461  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,631  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/130,829  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 827  
; TYPE: DNA  
; ORGANISM: Human  
US-10-208-018-56

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Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 479 GCATTGCCACTCCCATCTT 460

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; Publication No. US20030028923A1  
; GENERAL INFORMATION:  
; APPLICANT: Lardizabal, Kathryn D  
; APPLICANT: Hawkins, Deborah J  
; APPLICANT: Thompson, Gregory A  
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins  
; FILE REFERENCE: 16515.143  
; CURRENT APPLICATION NUMBER: US/10/121,857  
; CURRENT FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 09/345,461  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,631  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/130,829  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: murine  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(885)  
; OTHER INFORMATION: unsure at all n locations  
US-10-121-857-60

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Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
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Db 482 GCATTGCCACTCCCATCTT 463

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; Sequence 60, Application US/10208018  
; Publication No. US20030115632A1  
; GENERAL INFORMATION:  
; APPLICANT: Lardizabal, Kathryn D  
; APPLICANT: Hawkins, Deborah J  
; APPLICANT: Thompson, Gregory A  
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins  
; FILE REFERENCE: 16515.155  
; CURRENT APPLICATION NUMBER: US/10/208,018  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US 10/121,857  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 09/345,461  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,631  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/130,829  
; PRIOR FILING DATE: 1999-04-23  
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; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: murine  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(885)  
; OTHER INFORMATION: unsure at all n locations  
US-10-208-018-60

Query Match 100.0%; Score 20; DB 15; Length 885;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 482 GCATTGCCACTCCCATCTT 463

RESULT 8  
US-10-307-817-539  
; Sequence 539, Application US/10307817  
; Publication No. US20040056338A1  
; GENERAL INFORMATION:  
; APPLICANT: Ague et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: ChraSeqList version 0.1  
; SEQ ID NO 539  
; LENGTH: 1030  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-307-817-539

Query Match 100.0%; Score 20; DB 18; Length 1030;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 274 GCATTGCCACTCCCATCTT 293

RESULT 9  
US-10-307-817-538

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; Sequence 538, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: Curaseq1st version 0.1
; SEQ ID NO 538
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-307-817-538

Query Match          100.0%; Score 20; DB 18; Length 1077;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      384 GCATTGCCACTCCCATTCCTT 403

RESULT 10
US-09-794-715A-3/C
; Sequence 3, Application US/09794715A
; Patent No. US20020119138A1
; GENERAL INFORMATION:
; APPLICANT: Cases, Sylvaine
; APPLICANT: Stone, Scot
; APPLICANT: Zhou, Ping
; APPLICANT: Farese, Robert V.
; TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
; TITLE OF INVENTION: (DGAT2a)
; FILE REFERENCE: 6510240US1
; CURRENT APPLICATION NUMBER: US/09/794,715A
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1137
; OTHER INFORMATION: n = A,T,C or G
US-09-794-715A-3

Query Match          100.0%; Score 20; DB 9; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATTGCCACTCCCATTCCTT 20
        |||||
Db      698 GCATTGCCACTCCCATTCCTT 679

RESULT 11
US-10-278-733-8/C
; Sequence 8, Application US/10278733
; Publication No. US20030100480A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Steven
; APPLICANT: Chen, Hubert
; APPLICANT: Farese, Robert V Jr
; TITLE OF INVENTION: Methods and compositions for modulating
; FILE REFERENCE: UCAL-105C1P4
; CURRENT APPLICATION NUMBER: US/10/278,733
; CURRENT FILING DATE: 2002-10-21
```

```
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1167)
; OTHER INFORMATION: Homo sapiens DGAT 2 coding sequence
US-10-278-733-8

Query Match          100.0%; Score 20; DB 15; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATTGCCACTCCCATTCCTT 20
        |||||
Db      698 GCATTGCCACTCCCATTCCTT 679

RESULT 12
US-10-208-018-97/C
; Sequence 97, Application US/10208018
; Publication No. US20030115632A1
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.155
; CURRENT APPLICATION NUMBER: US/10/208,018
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 10/121,857
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Murinae gen. sp.
US-10-208-018-97

Query Match          100.0%; Score 20; DB 15; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATTGCCACTCCCATTCCTT 20
        |||||
Db      698 GCATTGCCACTCCCATTCCTT 679

RESULT 13
US-10-208-018-111/C
; Sequence 111, Application US/10208018
; Publication No. US20030115632A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.155
; CURRENT APPLICATION NUMBER: US/10/208.018
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 10/121,857
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-208-018-111

Query Match          100.0%; Score 20; DB 15; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 GCATTGCCACTCCCATCTT 20
Db 698 GCATTGCCACTCCCATCTT 679
```

## RESULT 14

```
US-10-208-018-126/c
; Sequence 126, Application US/10208018
; Publication No. US20030115632a1
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.155
; CURRENT APPLICATION NUMBER: US/10/208.018
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 10/121,857
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Murinae gen. sp.
US-10-208-018-126
```

```
Query Match          100.0%; Score 20; DB 15; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 GCATTGCCACTCCCATCTT 20
Db 698 GCATTGCCACTCCCATCTT 679
```

```
RESULT 15
US-10-046-924-3/c
; Sequence 3, Application US/10046924
; Publication No. US20030124126a1
```

```

; GENERAL INFORMATION:
; APPLICANT: Cases, Sylvaine
; APPLICANT: Stone, Scot
; APPLICANT: Zhou, Ping
; APPLICANT: Farese, Robert V.
; APPLICANT: Chi-Liang Eric Yen
; TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
; FILE REFERENCE: UCAL240CIP2
; CURRENT APPLICATION NUMBER: US/10/046.924
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 60/271,307
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/794,715
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1167)
; OTHER INFORMATION: n = A,T,C or G
US-10-046-924-3
```

```
Query Match          100.0%; Score 20; DB 15; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 GCATTGCCACTCCCATCTT 20
Db 698 GCATTGCCACTCCCATCTT 679
```

```
RESULT 16
US-10-286-581-3/c
; Sequence 3, Application US/10286581
; Publication No. US20030161831a1
; GENERAL INFORMATION:
; APPLICANT: Cases, Sylvaine
; APPLICANT: Stone, Scot
; APPLICANT: Zhou, Ping
; APPLICANT: Farese, Robert V.
; APPLICANT: Chi-Liang, Eric Yen
; TITLE OF INVENTION: Mono- and diacylglycerol acyltransferases
; FILE REFERENCE: UCAL240CIP2
; CURRENT APPLICATION NUMBER: US/10/286.581
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/271,307
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/794,715
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 10/046,924
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1167)
; OTHER INFORMATION: n = A,T,C or G
US-10-286-581-3
```

```
Query Match          100.0%; Score 20; DB 15; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 698 GCATTGCCACTCCCATCTT 679

RESULT 17  
US-10-446-441-3/c  
; Sequence 3, Application US/10446441  
; Publication No. US20030202968A1  
; GENERAL INFORMATION:  
; APPLICANT: Cases, Sylvaine  
; APPLICANT: Stone, Scot  
; APPLICANT: Zhou, Ping  
; APPLICANT: Farese, Robert V.  
; TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a  
; FILE REFERENCE: UCAL-240CON  
; CURRENT APPLICATION NUMBER: US/10/446,441  
; PRIOR FILING DATE: 2003-05-27  
; PRIOR APPLICATION NUMBER: US 09/794,715  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/271,307  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1167  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1137  
; OTHER INFORMATION: n = A,T,C or G  
US-10-446-441-3

Query Match 100.0%; Score 20; DB 17; Length 1167;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 698 GCATTGCCACTCCCATCTT 679

RESULT 18  
US-10-945-738-3/c  
; Sequence 3, Application US/10945738  
; Publication No. US20050106697A1  
; GENERAL INFORMATION:  
; APPLICANT: Cases, Sylvaine  
; APPLICANT: Stone, Scot  
; APPLICANT: Zhou, Ping  
; APPLICANT: Farese, Robert V.  
; APPLICANT: Chi-liang Eric Yen  
; TITLE OF INVENTION: Mono- and diacylglycerol acyltransferases  
; FILE REFERENCE: UCAL-240CON2  
; CURRENT APPLICATION NUMBER: US/10/945,738  
; PRIOR FILING DATE: 2004-09-20  
; PRIOR APPLICATION NUMBER: 10/286,581  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: 60/271,307  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/794,715  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 10/046,924  
; PRIOR FILING DATE: 2002-01-14  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1167  
; TYPE: DNA  
; ORGANISM: Mus musculus

; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(1167)  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1137  
; OTHER INFORMATION: n = A,T,C or G  
US-10-945-738-3

Query Match 100.0%; Score 20; DB 21; Length 1167;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 698 GCATTGCCACTCCCATCTT 679

RESULT 19  
US-10-307-817-103/c  
; Sequence 103, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 103  
; LENGTH: 1172  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)...(1169)  
US-10-307-817-103

Query Match 100.0%; Score 20; DB 18; Length 1172;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 703 GCATTGCCACTCCCATCTT 684

RESULT 20  
US-10-307-817-101/c  
; Sequence 101, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 101  
; LENGTH: 1189  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)...(1186)  
US-10-307-817-101

Query Match 100.0%; Score 20; DB 18; Length 1189;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 702 GCATTGCCACTCCCATCTT 683

RESULT 21  
US-10-307-817-107/c  
; Sequence 107, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 107  
; LENGTH: 1189  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)..(1186)  
US-10-307-817-107

Query Match 100.0%; Score 20; DB 18; Length 1189;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 702 GCATTGCCACTCCCATCTT 683

RESULT 22  
US-10-307-817-93/c  
; Sequence 93, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 93  
; LENGTH: 1191  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1188)  
US-10-307-817-93

Query Match 100.0%; Score 20; DB 18; Length 1191;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 722 GCATTGCCACTCCCATCTT 703

RESULT 23  
US-10-307-817-97/c  
; Sequence 97, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 97  
; LENGTH: 1191  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1188)  
US-10-307-817-97

Query Match 100.0%; Score 20; DB 18; Length 1191;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 722 GCATTGCCACTCCCATCTT 703

RESULT 24  
US-10-307-817-105/c  
; Sequence 105, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 105  
; LENGTH: 1198  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (14)..(1117)  
US-10-307-817-105

Query Match 100.0%; Score 20; DB 18; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||  
Db 711 GCATTGCCACTCCCATCTT 692

RESULT 25  
US-10-307-817-99/c  
; Sequence 99, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 99  
; LENGTH: 1207  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1194)  
US-10-307-817-99

Query Match 100.0%; Score 20; DB 18; Length 1207;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
|||||  
Db 710 GCATTGCCACTCCCATTTCTT 691

RESULT 26  
US-10-307-817-95/c  
; Sequence 95, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 95  
; LENGTH: 1230  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (8)..(1168)  
US-10-307-817-95

Query Match 100.0%; Score 20; DB 18; Length 1230;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
|||||  
Db 702 GCATTGCCACTCCCATTTCTT 683

RESULT 27  
US-10-307-817-540/c  
; Sequence 540, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 540  
; LENGTH: 1230  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-307-817-540

Query Match 100.0%; Score 20; DB 18; Length 1230;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
|||||  
Db 702 GCATTGCCACTCCCATTTCTT 683

RESULT 28  
US-09-794-715A-1/c  
; Sequence 1, Application US/09794715A  
; Patent No. US20020119138A1  
; GENERAL INFORMATION:  
; APPLICANT: Cases, Sylvaine

; APPLICANT: Stone, Scot  
; APPLICANT: Zhou, Ping  
; APPLICANT: Farese, Robert V.  
; TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a  
; FILE REFERENCE: (DGAT2a)  
; FILE REFERENCE: 6510240US1  
; CURRENT APPLICATION NUMBER: US/09/794,715A  
; CURRENT FILING DATE: 2001-02-26  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1231  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-794-715A-1

Query Match 100.0%; Score 20; DB 9; Length 1231;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
|||||  
Db 702 GCATTGCCACTCCCATTTCTT 683

RESULT 29  
US-10-046-924-1/c  
; Sequence 1, Application US/10046924  
; Publication No. US20030124126A1  
; GENERAL INFORMATION:  
; APPLICANT: Cases, Sylvaine  
; APPLICANT: Stone, Scot  
; APPLICANT: Zhou, Ping  
; APPLICANT: Farese, Robert V.  
; APPLICANT: Chi-Liang Eric Yen  
; TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a  
; FILE REFERENCE: (DGAT2a)  
; FILE REFERENCE: UCAL240CIP  
; CURRENT APPLICATION NUMBER: US/10/046,924  
; CURRENT FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: 60/271,307  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/794,715  
; PRIOR FILING DATE: 2001-02-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1231  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-046-924-1

Query Match 100.0%; Score 20; DB 15; Length 1231;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
|||||  
Db 702 GCATTGCCACTCCCATTTCTT 683

RESULT 30  
US-10-286-581-1/c  
; Sequence 1, Application US/10286581  
; Publication No. US20030161831A1  
; GENERAL INFORMATION:  
; APPLICANT: Cases, Sylvaine  
; APPLICANT: Stone, Scot  
; APPLICANT: Zhou, Ping  
; APPLICANT: Farese, Robert V.  
; APPLICANT: Chi-Liang, Eric Yen  
; TITLE OF INVENTION: Mono- and diacylglycerol acyltransferases  
; and methods of use thereof



FILE REFERENCE: UCAL240CIP2  
CURRENT APPLICATION NUMBER: US/10/286,581  
CURRENT FILING DATE: 2002-10-31  
PRIOR APPLICATION NUMBER: 60/271,307  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/794,715  
PRIOR FILING DATE: 2001-02-26  
PRIOR APPLICATION NUMBER: 10/046,924  
PRIOR FILING DATE: 2002-01-14  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1231  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-286-581-1

Query Match 100.0%; Score 20; DB 16; Length 1231;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 702 GCATTGCCACTCCCATCTT 683

RESULT 31  
US-10-446-441-1/c  
Sequence 1, Application US/10446441  
Publication No. US20030202968A1  
GENERAL INFORMATION:  
APPLICANT: Cases, Sylvaine  
APPLICANT: Stone, Scot  
APPLICANT: Zhou, Ping  
APPLICANT: Farese, Robert V.  
TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a  
FILE REFERENCE: UCAL-240CON  
CURRENT APPLICATION NUMBER: US/10/446,441  
CURRENT FILING DATE: 2003-05-27  
PRIOR APPLICATION NUMBER: US 09/794,715  
PRIOR FILING DATE: 2001-02-26  
PRIOR APPLICATION NUMBER: 60/271,307  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1231  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-446-441-1

Query Match 100.0%; Score 20; DB 17; Length 1231;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 702 GCATTGCCACTCCCATCTT 683

RESULT 32  
US-10-945-738-1/c  
Sequence 1, Application US/10945738  
Publication No. US20050106697A1  
GENERAL INFORMATION:  
APPLICANT: Cases, Sylvaine  
APPLICANT: Stone, Scot  
APPLICANT: Zhou, Ping  
APPLICANT: Farese, Robert V.  
APPLICANT: Chi-Liang Eric Yen  
TITLE OF INVENTION: Mono- and diacylglycerol acyltransferases  
TITLE OF INVENTION: and methods of use thereof

FILE REFERENCE: UCAL-240CON2  
CURRENT APPLICATION NUMBER: US/10/945,738  
CURRENT FILING DATE: 2004-09-20  
PRIOR APPLICATION NUMBER: 10/266,581  
PRIOR FILING DATE: 2002-10-31  
PRIOR APPLICATION NUMBER: 60/271,307  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/794,715  
PRIOR FILING DATE: 2001-02-26  
PRIOR APPLICATION NUMBER: 10/046,924  
PRIOR FILING DATE: 2002-01-14  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1231  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-945-738-1

Query Match 100.0%; Score 20; DB 21; Length 1231;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 702 GCATTGCCACTCCCATCTT 683

RESULT 33  
US-10-046-924-18/c  
Sequence 18, Application US/10046924  
Publication No. US20030124126A1  
GENERAL INFORMATION:  
APPLICANT: Cases, Sylvaine  
APPLICANT: Stone, Scot  
APPLICANT: Zhou, Ping  
APPLICANT: Farese, Robert V.  
APPLICANT: Chi-Liang Eric Yen  
TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a  
FILE REFERENCE: UCAL240CIP  
CURRENT APPLICATION NUMBER: US/10/046,924  
CURRENT FILING DATE: 2003-01-14  
PRIOR APPLICATION NUMBER: 60/271,307  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/794,715  
PRIOR FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 1233  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-046-924-18

Query Match 100.0%; Score 20; DB 15; Length 1233;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 705 GCATTGCCACTCCCATCTT 686

RESULT 34  
US-10-286-581-18/c  
Sequence 18, Application US/10286581  
Publication No. US20030161831A1  
GENERAL INFORMATION:  
APPLICANT: Cases, Sylvaine  
APPLICANT: Stone, Scot  
APPLICANT: Zhou, Ping  
APPLICANT: Farese, Robert V.

```
/ APPLICANT: Chi-liang, Eric Yen
/ TITLE OF INVENTION: Mono- and diacylglycerol acyltransferases
/ FILE REFERENCE: UCA1240CIP2
/ CURRENT APPLICATION NUMBER: US/10/286,581
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: 60/271,307
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 09/794,715
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 10/046,924
/ PRIOR FILING DATE: 2002-01-14
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 1233
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-286-581-18
```

```
Query Match          100.0%; Score 20; DB 16; Length 1233;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GCATTGCCACTCCCATCTT 20
        |||
Db       705 GCATTGCCACTCCCATCTT 686
```

```
RESULT 35
US-10-945-738-18/C
/ Sequence 18, Application US/10945738
/ Publication No. US20050106697A1
/ GENERAL INFORMATION:
/ APPLICANT: Cases, Sylvaine
/ APPLICANT: Stone, Scott
/ APPLICANT: Zhou, Ping
/ APPLICANT: Farese, Robert V.
/ APPLICANT: Chi-liang, Eric Yen
/ TITLE OF INVENTION: Mono- and diacylglycerol acyltransferases
/ FILE REFERENCE: UCA1-240CON2
/ CURRENT APPLICATION NUMBER: US/10/945,738
/ CURRENT FILING DATE: 2004-09-20
/ PRIOR APPLICATION NUMBER: 10/286,581
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: 60/271,307
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 09/794,715
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 10/046,924
/ PRIOR FILING DATE: 2002-01-14
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 1233
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-945-738-18
```

```
Query Match          100.0%; Score 20; DB 21; Length 1233;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GCATTGCCACTCCCATCTT 20
        |||
Db       705 GCATTGCCACTCCCATCTT 686
```

```
RESULT 36
US-10-172-118-2665
/ Sequence 2665, Application US/10172118
/ Publication No. US20030224374A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dai, Hongyue
/ APPLICANT: He, Yudong
/ APPLICANT: Linsley, Peter
/ APPLICANT: Mao, Mao
/ APPLICANT: Roberts, Chris
/ APPLICANT: Van 't Veer, Laura
/ APPLICANT: Van de Vijver, Marc
/ APPLICANT: Bernards, Rene
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
/ FILE REFERENCE: 9301-175-999
/ CURRENT APPLICATION NUMBER: US/10/172,118
/ CURRENT FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 60/380,770
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 2665
/ LENGTH: 1510
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: Contigs58260
/ DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2665
```

```
Query Match          100.0%; Score 20; DB 17; Length 1510;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GCATTGCCACTCCCATCTT 20
        |||
Db       1491 GCATTGCCACTCCCATCTT 1510
```

```
RESULT 37
US-10-342-887-2665
/ Sequence 2665, Application US/10342887
/ Publication No. US20040058340A1
/ GENERAL INFORMATION:
/ APPLICANT: Dai, Hongyue
/ APPLICANT: He, Yudong
/ APPLICANT: Linsley, Peter S.
/ APPLICANT: Mao, Mao
/ APPLICANT: Roberts, Christopher J.
/ APPLICANT: Van 't Veer, Laura Johanna
/ APPLICANT: Van de Vijver, Marc J.
/ APPLICANT: Bernards, Rene
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
/ FILE REFERENCE: 9301-188-999
/ CURRENT APPLICATION NUMBER: US/10/342,887
/ CURRENT FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: 60/298,918
/ PRIOR FILING DATE: 2001-06-18
/ PRIOR APPLICATION NUMBER: 60/380,710
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 10/172,118
/ PRIOR FILING DATE: 2002-06-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 2665
/ LENGTH: 1510
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-342-887-2665
```

```
Query Match          100.0%; Score 20; DB 18; Length 1510;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GCATTGCCACTCCCATCTT 20
        |||
Db       1491 GCATTGCCACTCCCATCTT 1510
```

RESULT 38  
US-09-946-374-291/c  
Sequence 291, Application US/09946374  
Publication No. US20030073129A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godewski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15

PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484

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/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 60/102487
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 60/102570
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 60/102571
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 60/102684
/ PRIOR FILING DATE: 1998-10-01
/ PRIOR APPLICATION NUMBER: 60/102687
/ PRIOR FILING DATE: 1998-10-01
/ PRIOR APPLICATION NUMBER: 60/102965
/ PRIOR FILING DATE: 1998-10-02
/ PRIOR APPLICATION NUMBER: 60/103258
/ PRIOR FILING DATE: 1998-10-06
/ PRIOR APPLICATION NUMBER: 60/103314
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103315
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103328
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103395
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103396
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103401
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103449
/ PRIOR FILING DATE: 1998-10-06
/ PRIOR APPLICATION NUMBER: 60/103633
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/103678
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/103679
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/103711
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/104257
/ PRIOR FILING DATE: 1998-10-14
/ PRIOR APPLICATION NUMBER: 60/104987
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: 60/105000
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: 60/105002
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: 60/105104
/ PRIOR FILING DATE: 1998-10-21
/ PRIOR APPLICATION NUMBER: 60/105169
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: 60/105266
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: 60/105693
/ PRIOR FILING DATE: 1998-10-26
/ PRIOR APPLICATION NUMBER: 60/105694
/ PRIOR FILING DATE: 1998-10-26
/ PRIOR APPLICATION NUMBER: 60/105807
```

```
Query Match 100.0%; Score 20; DB 10; Length 1570;
Best Local Similarity 100.0%; Pred.No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GCATTGCCACTCCATTCTT 20
Db 882 GCATTGCCACTCCATTCTT 863
```

```
RESULT 39
US-10-052-586-335/C
; Sequence 335, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
```

```
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C1
/ CURRENT APPLICATION NUMBER: US/10/052,586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059266
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063121
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063486
/ PRIOR FILING DATE: 1997-10-21
/ PRIOR APPLICATION NUMBER: 60/063540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063564
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063734
/ PRIOR FILING DATE: 1997-10-29
/ PRIOR APPLICATION NUMBER: 60/063870
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066120
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: 60/066466
/ PRIOR FILING DATE: 1997-11-24
/ PRIOR APPLICATION NUMBER: 60/066772
/ PRIOR FILING DATE: 1997-11-24
/ PRIOR APPLICATION NUMBER: 60/069335
/ PRIOR FILING DATE: 1997-12-11
/ PRIOR APPLICATION NUMBER: 60/069425
/ PRIOR FILING DATE: 1997-12-12
/ PRIOR APPLICATION NUMBER: 60/069870
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/068017
/ PRIOR FILING DATE: 1997-12-18
/ PRIOR APPLICATION NUMBER: 60/077450
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 60/077632
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077649
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/078886
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/078939
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079664
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079786
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/080107
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080194
```

;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080327  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/080333  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/081049  
;; PRIOR FILING DATE: 1998-04-08  
;; PRIOR APPLICATION NUMBER: 60/081070  
;; PRIOR FILING DATE: 1998-04-08  
;; PRIOR APPLICATION NUMBER: 60/081195  
;; PRIOR FILING DATE: 1998-04-09  
;; PRIOR APPLICATION NUMBER: 60/081838  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/082568  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082569  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082704  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082797  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083496  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084639  
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;; PRIOR APPLICATION NUMBER: 60/084640  
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;; PRIOR APPLICATION NUMBER: 60/084643  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
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;; PRIOR APPLICATION NUMBER: 60/085580  
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;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
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;; PRIOR FILING DATE: 1998-05-18  
;; PRIOR APPLICATION NUMBER: 60/086392  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/086486  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087098  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087208  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087609  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088025  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04

;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088555  
;; PRIOR FILING DATE: 1998-06-09  
;; PRIOR APPLICATION NUMBER: 60/088722  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088740  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088811  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088824  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088825  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088863  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089090  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089512  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089538  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 20; DB 13; Length 1570;  
Best Local Similarity 100.0%; Fred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GCATTGCCACTCCCATCTT 20  
Db 882 GCATTGCCACTCCCATCTT 863

RESULT 40  
US-10-174-590-335/c  
;; Sequence 335, Application US//10174590  
;; Publication No. US20030008352A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Tian  
;; APPLICANT: Deenoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.

```

; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-335

Query Match          100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTTCTT 20
Db 882 GCATTGCCACTCCCATTTCTT 863

RESULT 41
US-10-176-758-335/c
; Sequence 335, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-335

Query Match          100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTTCTT 20
Db 882 GCATTGCCACTCCCATTTCTT 863

RESULT 42
US-10-175-737-335/c
; Sequence 335, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-335

Query Match          100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTTCTT 20
Db 882 GCATTGCCACTCCCATTTCTT 863
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```

; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-335

Query Match          100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTTCTT 20
Db 882 GCATTGCCACTCCCATTTCTT 863

RESULT 43
US-10-174-581-335/c
; Sequence 335, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/05263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
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PRIOR FILING DATE: 1997-10-31	PRIOR APPLICATION NUMBER: 60/664103
PRIOR FILING DATE: 1997-10-31	PRIOR APPLICATION NUMBER: 60/665311
PRIOR FILING DATE: 1997-11-13	PRIOR APPLICATION NUMBER: 60/666120
PRIOR FILING DATE: 1997-11-21	PRIOR APPLICATION NUMBER: 60/666466
PRIOR FILING DATE: 1997-11-24	PRIOR APPLICATION NUMBER: 60/667722
PRIOR FILING DATE: 1997-11-24	PRIOR APPLICATION NUMBER: 60/669335
PRIOR FILING DATE: 1997-12-11	PRIOR APPLICATION NUMBER: 60/669425
PRIOR FILING DATE: 1997-12-11	PRIOR APPLICATION NUMBER: 60/669870
PRIOR FILING DATE: 1997-12-17	PRIOR APPLICATION NUMBER: 60/668017
PRIOR FILING DATE: 1997-12-18	PRIOR APPLICATION NUMBER: 60/677450
PRIOR FILING DATE: 1997-12-12	PRIOR APPLICATION NUMBER: 60/677632
PRIOR FILING DATE: 1998-03-11	PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11	PRIOR APPLICATION NUMBER: 60/078866
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080353
PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/080409
PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05	PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084639

PRIOR APPLICATION NUMBER:	60/084643-0
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084643-3
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085573-2
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085579-7
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085580-0
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085582-8
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700-0
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/086023-2
PRIOR FILING DATE:	1998-05-18
PRIOR APPLICATION NUMBER:	60/086392-2
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087208-0
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087609-0
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087759-8
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087822-0
PRIOR FILING DATE:	1998-06-03
PRIOR APPLICATION NUMBER:	60/088023-5
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088028-8
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088029-2
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088033-6
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088167-8
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088212-2
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088217-1
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088326-6
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088655-5
PRIOR FILING DATE:	1998-06-09
PRIOR APPLICATION NUMBER:	60/088722-2
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088738-8
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088740-4
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088811-1
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088824-2
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088825-5
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088826-2
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088861-6
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/088863-1
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/088887-6
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/089090-0
PRIOR FILING DATE:	1998-06-12
PRIOR APPLICATION NUMBER:	60/089105-0

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; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
```

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Query Match          100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 GCATTGCCACTCCCATTTCTT 20
        |||||
Db      882 GCATTGCCACTCCCATTTCTT 863
```

## RESULT 44

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US-10-176-483-335/c
; Sequence 335, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-483-335
```

```
Query Match          100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GCATTGCCACTCCCATTTCTT 20
        |||||
Db      882 GCATTGCCACTCCCATTTCTT 863
```

## RESULT 45

```
US-10-176-749-335/c
; Sequence 335, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
```

```
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-335
```

```
Query Match          100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GCATTGCCACTCCCATTTCTT 20
        |||||
Db      882 GCATTGCCACTCCCATTTCTT 863
```

```
Search completed: August 5, 2005, 02:33:27
Job time : 621 secs
```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 16:53:28 ; Search time 3141 Seconds

(without alignments)  
242.370 Million cell updates/sec

Title: US-10-643-801A-35

Perfect score: 20

Sequence: 1 gcatgcacccatctctc 20

Scoring table: OLIGO\_NUC

Searched: 34239544 seqs, 19032134700 residues

Word size : 8

Total number of hits satisfying chosen parameters: 6604802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

EST: \*  
1: gb\_eact1: \*  
2: gb\_eact2: \*  
3: gb\_hcc: \*  
4: gb\_eact3: \*  
5: gb\_eact4: \*  
6: gb\_eact5: \*  
7: gb\_eact6: \*  
8: gb\_gse81: \*  
9: gb\_gse82: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	288	2	BF236347 602025981
2	20	100.0	291	4	BG687855 315149 BA
3	20	100.0	293	7	H25606
4	20	100.0	300	4	BG190696
5	20	100.0	324	9	CE638239
6	20	100.0	415	1	AA674642
7	20	100.0	421	2	BF430191
8	20	100.0	426	2	BF147241
9	20	100.0	435	7	R69540
10	20	100.0	450	1	AA880955
11	20	100.0	466	1	AA797343
12	20	100.0	502	2	BE482224
13	20	100.0	503	6	CA536347
14	20	100.0	508	2	BE479873
15	20	100.0	511	4	BG741469
16	20	100.0	534	2	BE625643
17	20	100.0	540	2	BE014044
18	20	100.0	559	4	BM851596
19	20	100.0	586	7	CF106297
20	20	100.0	590	4	BG696693
21	20	100.0	592	4	BP316675
22	20	100.0	615	5	BP382116
23	20	100.0	621	7	CK970536
24	20	100.0	625	4	BG484381

25	20	100.0	631	2	BF660115
26	20	100.0	632	6	CA535709
27	20	100.0	646	6	CB267111
28	20	100.0	653	4	B1144404
29	20	100.0	653	4	B1908609
30	20	100.0	677	2	BF237046
31	20	100.0	698	2	BF236900
32	20	100.0	710	4	B1332607
33	20	100.0	718	4	B1915586
34	20	100.0	732	4	BG695886
35	20	100.0	743	4	BG194285
36	20	100.0	743	4	BG695953
37	20	100.0	747	7	CR383515
38	20	100.0	762	4	BF980113
39	20	100.0	776	4	BG739895
40	20	100.0	781	4	BG697487
41	20	100.0	789	4	BG199090
42	20	100.0	800	4	BG212376
43	20	100.0	809	4	BG685428
44	20	100.0	809	4	B1247050
45	20	100.0	816	5	BU541989
46	20	100.0	817	4	B1145888
47	20	100.0	819	5	BU939162
48	20	100.0	822	5	BU422455
49	20	100.0	857	4	BG681732
50	20	100.0	890	4	BM044041
51	20	100.0	897	4	BG740407
52	20	100.0	921	2	BF235987
53	20	100.0	930	6	CB201584
54	20	100.0	985	4	B1257050
55	20	100.0	1021	5	BM922778
56	20	100.0	1167	9	AY413823
57	20	100.0	1167	9	AY413825
58	20	100.0	1458	3	AK016660
59	20	100.0	2262	3	AK002443
60	20	100.0	5929	3	CR749377
61	20	100.0	95.0	4	BG694175
62	19	95.0	955	4	B1329751
63	19	95.0	1068	5	BU432841
64	18	90.0	648	4	B1148931
65	18	90.0	802	5	BU240541
66	17	85.0	328	6	CB544923
67	17	85.0	400	5	BP074578
68	17	85.0	412	5	BP070330
69	17	85.0	436	5	BP048604
70	17	85.0	485	5	BP057725
71	17	85.0	508	5	BP032369
72	17	85.0	522	5	BP050447
73	17	85.0	609	9	CL360447
74	17	85.0	737	6	CA254078
75	17	85.0	856	9	CC542723
76	16	80.0	253	8	AZ222921
77	16	80.0	376	8	BH833646
78	16	80.0	441	6	BY646381
79	16	80.0	524	5	BQ623490
80	16	80.0	568	9	FR0024959
81	16	80.0	588	5	BQ488822
82	16	80.0	654	1	AL869177
83	16	80.0	658	1	AL655054
84	16	80.0	686	9	AG086546
85	16	80.0	689	9	AG086766
86	16	80.0	705	7	CE176858
87	16	80.0	798	7	CN277508
88	16	80.0	800	4	BG199398
89	16	80.0	843	4	CL944456
90	16	80.0	865	4	B1757445
91	16	80.0	983	5	BQ649756
92	16	80.0	983	7	CR293208
93	16	80.0	1071	5	BM906576
94	16	80.0	1684	4	BG028155
95	15	75.0	174	1	AI834935
96	15	75.0	192	2	BB213350
97	15	75.0	227	7	NS4232

BF660115	maa27908.
CA535709	C0223802.
CB267111	1006017 H
B1144404	602908548
B1908609	603066720
BF237046	602026681
BF236900	602026519
B1332607	602980747
B1915586	603176945
BG695886	602657850
BG194285	RST13430
BG695953	602657968
CR383515	CR383515
BF980113	602288115
BG739895	602630838
BG697487	602660680
BG199090	RST8128 A
BG212376	RST31963
BG685428	602783545
B1247050	602960387
BU541989	AGENCOURT
B1145888	602911193
BU939162	AGENCOURT
BU422455	603230757
BG681732	602627853
BM044041	603621091
BG740407	602634184
BF235987	602025672
CB201584	AGENCOURT
B1257050	602978893
BM922778	AGENCOURT
AY413823	Homo sapi
AY413825	Mus muscu
AK016660	Mus muscu
AK002443	Mus muscu
CR749377	Homo sapi
BG694175	345227 BA
B1329751	602985095
BU432841	603222475
B1148931	602908974
BU240541	603321673
CB544923	AMGNUNC:IS
BP074578	BP074578
BP070330	BP070330
BP048604	BP048604
BP057725	BP057725
BP032369	BP032369
BP050447	BP050447
CL360447	RPC144_33
CA254078	SCRFL410
CC542723	CR240 424
BA222921	RPCI-23-9
BH833646	BAEPP35-F
BY646381	BY646381
BQ623490	USDA-FP-0
FR0024959	F.rubripide
BQ488822	89-E8455-
AL869177	AL869177
AL655054	AL655054
AG086546	Pan trogl
AG086766	Pan trogl
CE176858	CR176858
CN277508	170004180
BG199398	RST18681
CL944456	OB1F8B003
B1757445	603029383
BQ649756	AGENCOURT
CR293208	CR293208
BM906576	AGENCOURT
BG028155	602293217
AI834935	UT-M-ANI-
BB213350	BB213350
NS4232	Y203501.r1

98 15 75.0 238 6 CA909075 PCS007883  
99 15 75.0 268 6 CA909073 PCS04651  
100 15 75.0 273 2 BB373219 BB373219

## ALIGNMENTS

RESULT 1  
BP236347/c 288 bp mRNA linear EST 14-NOV-2000  
LOCUS 602025951F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:4160948 5',  
DEFINITION mRNA sequence.  
ACCESSION BP236347  
VERSION BP236347.1 GI:11149879  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE 1 (bases 1 to 288)  
JOURNAL NIH-WGC http://mgc.nci.nih.gov/  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
founded distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM9441 row: b column: 21  
High quality sequence stop: 288.

FEATURES  
source

1..288  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4160948"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_11b="NCI\_CGAP\_Li9"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

Query Match 100.0%; Score 20; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
Db 82 GCATTGCCACTCCCATCTT 63

RESULT 2  
BG687855/c 291 bp mRNA linear EST 27-MAR-2003  
LOCUS 335149 BANC SBOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BG687855  
VERSION BG687855.1 GI:13929656  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 291)  
Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,

Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.  
and Quackenbush,J.  
Analysis of bovine mammary gland EST and functional annotation of  
the Bos taurus gene index  
Mamm. Genome 13 (7), 373-379 (2002)  
JOURNAL MEDLINE  
PUBMED 22335956  
12140684

COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACATCGACGAC  
Plate: 33 row: M column: 14  
Seq primer: ATTAGTGACATGAC.  
Location/Qualifiers  
1..291

FEATURES  
source

/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_11b="BANC SBOV"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 291;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
Db 239 GCATTGCCACTCCCATCTT 220

RESULT 3  
H25606/c 293 bp mRNA linear EST 10-JUL-1995  
LOCUS Y148C07.r1 Soares breast 3nbHst Homo sapiens cDNA clone  
DEFINITION IMAGE:161484 5', mRNA sequence.  
ACCESSION H25606  
VERSION H25606.1 GI:894729  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 293)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maier,M.,  
Parsons,J., Riklin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The Washt-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 676  
High quality sequence stops: 260  
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 676 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 260.

## FEATURES

## Source

1. 293  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:575637"  
/db\_xref="taxon:9606"  
/clone="IMAGE:161484"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares breast 3mbibac"  
/note="Organ: breast; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 293;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 20 GCATTGCCACTCCCATCTT 1

RESULT 4  
LOCUS BG190696 300 bp mRNA linear EST 21-APR-2001  
DEFINITION RST97770 Atherysa RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG190696  
VERSION BG190696.1 GI:13712383  
KEYWORDS EST.

SOURCE  
ORGANISM Homo sapiens (human)

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,  
Whitington,J., Letner,L., Costanzo,D., McElligott,K., Booser,S.,  
Mays,R., Smith,E., Veloso,N., Kika,A., Hees,J., Cothren,K., Lo,K.,  
Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random  
activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE  
JOURNAL MEDLINE  
PUBMED 11329013  
COMMENT  
Contact: Scott J. Cain  
Atherysa, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atherysa.com  
High quality sequence stop: 250.

## FEATURES

## Source

1. 300  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="HT1080"  
/clone\_lib="Atherysa RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 300;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 262 GCATTGCCACTCCCATCTT 243

RESULT 5  
LOCUS CE638239 324 bp DNA linear GSS 29-SEP-2003  
DEFINITION tigr-gss-dog-17000366770212 Dog Library Canis familiaris genomic,  
genomic survey sequence.

ACCESSION CE638239  
VERSION CE638239.1 GI:36955821  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.  
1 (bases 1 to 324)  
Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.

The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

TITLE  
JOURNAL MEDLINE  
PUBMED 14512627  
COMMENT  
Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.

FEATURES  
Source  
Location/Qualifiers  
1. 324  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BclXI; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 324;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
Db 74 GCATTGCCACTCCCATCTT 93

RESULT 6  
LOCUS AA674642 415 bp mRNA linear EST 28-NOV-1997  
DEFINITION vc02a10\_r1 Stragatene mouse diaphragm (#937303) Mus musculus cDNA  
clone IMAGE:1093050 5', mRNA sequence.  
ACCESSION AA674642  
VERSION AA674642.1 GI:2651879  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 415)  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Maria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:599282  
Seq primer: -28m13 rev1 RT from Amerham.  
Location/Qualifiers  
1..415  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1093050"  
/tissue\_type="diaphragm"  
/dev\_stage="adult"  
/lab\_host="SOLR (kanamycin resistant)"  
/clone\_lib="Stratagene mouse diaphragm (#937303)"  
/note="Organ: diaphragm; Vector: phage-script SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dt. Average insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTATTTTATTTTATTTT 3'"

ORIGIN  
Query Match 100.0%; Score 20; DB 1; Length 415;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GCATTGCCACTCCATTCTT 20  
293 GCATTGCCACTCCATTCTT 274

RESULT 7  
LOCUS BF430191/c 421 bp mRNA linear EST 29-NOV-2000  
DEFINITION 256153 MARC BSM Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BF430191  
VERSION BF430191.1 GI:11442288  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 421)  
AUTHORS Warren, W.C., Tao, N., Allison, T., Wagner, S., Mathialagan, N., Kata, S., Johnson, J., Smith, T.P.L. and Womack, J.  
TITLE A survey of genes transcribed in bovine skeletal muscle  
JOURNAL Unpublished (2000)  
COMMENT Contact: Smith TP  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -mismatch 12 options.  
PCR primers  
FORWARD: GGAACAGCATGACCATG  
REVERSE: GTTATCCCTACTTAAAGG.  
Seq primer: AATTACCTACTTAAAGG.  
Location/Qualifiers  
1..421  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="Skeletal muscle"  
/lab\_host="XLOR"  
/clone\_lib="MARC BSM"  
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; Library obtained from Stratagene, catalog #937721. Library made from skeletal muscle of a two year old Holstein cow."

ORIGIN  
Query Match 100.0%; Score 20; DB 2; Length 421;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GCATTGCCACTCCATTCTT 20  
131 GCATTGCCACTCCATTCTT 112

RESULT 8  
LOCUS BF147241/c 426 bp mRNA linear EST 26-OCT-2000  
DEFINITION uw67f05.y1 Soares mammary\_gland NMLMG Mus musculus cDNA clone IMAGE:3467073 5' similar to TR:074850 O74850 HYPOTHETICAL 25.8 KD PROTEIN; , mRNA sequence.  
ACCESSION BF147241  
VERSION BF147241.1 GI:11028636  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 426)  
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Other ESTs: uw67f05.x1  
Contact: Robert Strauberg, Ph.D.  
Email: cgaps-remail.nih.gov  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:186433  
Seq primer: -40RP from Gibco  
High quality sequence stop: 344.  
Location/Qualifiers  
1..426  
/organism="Mus musculus"  
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/sex="female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"  
/clone\_lib="Soares mammary\_gland NMLMG"  
/note="Vector: pRT3D-pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dt) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bernaldo."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 0.37;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTGCCACTCCCATCTT 20  
 |||  
 347 GCATTGCCACTCCCATCTT 328

RESULT 9  
 R69540 435 bp mRNA linear EST 01-JUN-1995  
 R69540/c  
 LOCUS  
 DEFINITION Y182e11.r1 Soares breast 2NBHst Homo sapiens cDNA clone  
 IMAGE:155276 5', mRNA sequence.

ACCESSION  
 R69540  
 VERSION R69540.1 GI:843057  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Eutheria; Primates; Carnivora; Homnidae; Homo.  
 1 (bases 1 to 435)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevaekie, E., Waterston, R., Williamson, A., Woldmann, F. and  
 Wilson, R.  
 The Mashu-Merc EST Project  
 Unpublished (1995)  
 JOURNAL  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 905  
 High quality sequence stops: 350  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 905 Std Error: 0.00  
 Seq primer: M13RPI  
 High quality sequence stop: 350.

FEATURES  
 source  
 1. 435  
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 /db\_xref="GDB:571443"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:155276"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares breast 2NBHst"  
 /note="Organ: breast; Vector: pTV73D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3']  
 double-stranded cDNA was ligated to Eco RI adaptor  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of a modified pTV73 vector (Pharmacia).  
 Library went through one round of normalization to a Cot =  
 230. Library constructed by Bento Soares and M. Fatima  
 Bernaldo."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 0.37;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTGCCACTCCCATCTT 20

Db 20 GCATTGCCACTCCCATCTT 1  
 |||  
 166 GCATTGCCACTCCCATCTT 147

RESULT 10  
 AA880955/c 450 bp mRNA linear EST 26-MAR-1998  
 LOCUS  
 DEFINITION vx34c06.r1 Stragene mouse lung 937302 Mus musculus cDNA clone  
 IMAGE:1277098 5', similar to WP:001A11.2 CE14392; mRNA sequence.

ACCESSION  
 AA880955  
 VERSION AA880955.1 GI:2989938  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 450)  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Stepcie, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 The Mashu-HMI Mouse EST Project  
 Unpublished (1996)  
 JOURNAL  
 COMMENT Contact: Marra M/Mouse EST Project  
 Mashu-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouse@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:668898  
 Seq primer: -28m13 rev1 ET from Amersham  
 High quality sequence stop: 435.

FEATURES  
 source  
 1. 450  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6 x CBA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1277098"  
 /sex="female"  
 /tissue\_type="lung"  
 /dev\_stage="6-8 month old"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stragene mouse lung 937302"  
 /note="Organ: lung; Vector: pluscript SK-; Site 1:  
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dT. 6-8 month old female lung and 1.5 year old male  
 lung were source of mRNA. Average insert size: 1.5 Kb.  
 Un-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG  
 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 0.37;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTGCCACTCCCATCTT 20  
 |||  
 166 GCATTGCCACTCCCATCTT 147

RESULT 11  
 AA797343/c 466 bp mRNA linear EST 10-FEB-1998  
 LOCUS  
 DEFINITION vx23h05.r1 Soares mammary\_gland\_NbMKG Mus musculus cDNA clone  
 IMAGE:1244697 5', similar to TR:00181 00181 COSMID K07B1.; mRNA  
 sequence.

ACCESSION  
 AA797343  
 VERSION AA797343.1 GI:2860298



## POLYA=NO.

FEATURES  
source

Location/Qualifiers  
1. 503  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="NIA:CO233B11-5N"  
/tissue\_type="whole embryo. Including extraembryonic  
tissues at 7.5-days postcoitum"  
/dev\_stage="7.5-days postcoitum"  
/lab\_host="DH10B"  
/clone\_11b="NIA Mouse 7.5-dpc Whole Embryo cDNA library  
(Long)"  
/note="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (<http://198un.grc.nia.nih.gov/cDNA>). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were  
extracted from a pool of four embryos at 7.5-days  
postcoitum. Double-stranded cDNAs were synthesized with an  
Oligo(dT) primer (Invitrogen):  
5'-GGACTGAGTCTAGATCGGAGCGGCCCTTTTCTTTTCTTTT-3' from  
7 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to lone-linker L1-SalI, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Tag polymerase (Takara) with a primer SalI-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.2 kb. The library was constructed  
by Yulan Piao (NIA)."

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 503;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCATTCTT 20  
|||||  
Db 455 GCATTGCCACTCCATTCTT 436

RESULT 14  
BE479873/c 508 bp mRNA linear EST 27-MAR-2003  
LOCUS  
DEFINITION  
164726 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
BE479873  
VERSION  
BE479873.1 GI:9599406  
KEYWORDS  
EST.  
SOURCE  
Bos taurus (cow)  
ORGANISM  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE  
1 (bases 1 to 508)  
Sonstegard,T., Capuco,A.V., White,J., Van Tassel,J.C.P.,  
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.  
and Quackenbush,J.  
Analysis of bovine mammary gland EST and functional annotation of  
the Bos taurus gene index  
Mamm. Genome 13 (7), 373-379 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
22135956

COMMENT  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416  
Fax: 301 504 8414  
Email: [rsd@pilot.barc.usda.gov](mailto:rsd@pilot.barc.usda.gov)  
Single pass sequencing. Bases called and alt trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.

PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCACGACG  
Plate: 14 row: J column: 14  
Seq primer: ATTAGGTGACACTATG.

## FEATURES

source

Location/Qualifiers  
1. 508  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_11b="BARC 5BOV"  
/note="Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI;  
library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 508;  
Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCATTCTT 20  
|||||  
Db 164 GCATTGCCACTCCATTCTT 145

RESULT 15  
BG741469/c 511 bp mRNA linear EST 15-MAY-2001  
LOCUS  
DEFINITION  
602632261F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4777455 5',  
mRNA sequence.  
BG741469  
VERSION  
BG741469.1 GI:14052122  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NIA-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL10631 row: J column: 16  
High quality sequence stop: 509.

## FEATURES

source

Location/Qualifiers  
1. 511  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4777455"  
/lab\_host="DH10B (T1 phage-resistance)"  
/clone\_11b="NCI CGAP Skn3"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 511;  
 Best Local Similarity 100.0%; Pred. No. 0.37;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
 |||||  
 105 GCATTGCCACTCCCATCTT 86

## RESULT 16

BE625643/C

LOCUS BE625643 534 bp mRNA linear EST 24-AUG-2000  
 DEFINITION uc98b12.y2 Soares mammary gland NMLMG Mus musculus cDNA clone  
 IMAGE:3370463 5' similar to WP:R07B1.4 CELL882 ;, mRNA sequence.

ACCESSION BE625643  
 VERSION BE625643.1 GI:9906137  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 COMMENT Unpublished (1997)  
 Contact: Robert Strausberg, Ph. D.  
 Email: cgapbs-r@mail.nih.gov  
 This clone is available royalty-free through LML; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MW1:1080067  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 479.

## FEATURES

source  
 1. 534  
 Location/Qualifiers

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone\_xref="IMAGE:3370463"  
 /sex="female (lactating)"  
 /tissue\_type="mammary gland"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares mammary gland NMLMG"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; 1st strand cDNA was prepared from mammary  
 gland tissue from a lactating female, and was then primed  
 with a Not I - oligo(dT) primer. Double-stranded cDNA was  
 ligated to Eco RI adaptors (Pharmacia) digested with Not  
 I and cloned into the Not I and Eco RI sites of the  
 modified pT73 vector. Library is normalized. Library  
 was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 514;  
 Best Local Similarity 100.0%; Pred. No. 0.37;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
 |||||  
 47 GCATTGCCACTCCCATCTT 28

## RESULT 17

BE014044/C

LOCUS BE014044 540 bp mRNA linear EST 09-JUL-2000  
 DEFINITION 125617 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BE014044  
 VERSION BE014044.1 GI:8275035  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa

## REFERENCE

Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 1 (bases 1 to 540)  
 Fahrentkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,  
 Vallet,J., Wise,T., Rohrer,G.A., Petrea,G., Sultana,R.,  
 Quackenbush,J. and Keeler,J.W.  
 Porcine gene discovery by normalized cDNA-library sequencing and  
 EST cluster assembly  
 Mamm. Genome 13 (8), 475-478 (2002)

## TITLE

JOURNAL

MEDLINE

PUBMED

## COMMENT

Contract: Smith RPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and alt trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 18  
 and -minmatch 12 options.  
 PCR primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCAGTCACGACG  
 Plate: 54 row: C column: 20  
 Seq primer: ATTAGTGACACTATAG.

## FEATURES

source

1. 540  
 Location/Qualifiers  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 1Pig"  
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;  
 Library made from pooled tissue from day 11, 13, 15, 20,  
 and 30 embryos."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 0.37;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
 |||||  
 537 GCATTGCCACTCCCATCTT 518

## RESULT 18

BM851596/C

LOCUS BM851596 559 bp mRNA linear EST 06-MAR-2002  
 DEFINITION K-EST0132503 S21SNUS20 Homo sapiens cDNA clone S21SNUS20-34-H10 5',  
 mRNA sequence.

ACCESSION BM851596  
 VERSION BM851596.1 GI:19207995  
 KEYWORDS EST.

## SOURCE

ORGANISM

## REFERENCE

Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 559)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.

## TITLE

JOURNAL

COMMENT

21C Frontier Korean EST Project 2001  
 Unpublished (2002)  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: Yongsung@mail.krribb.re.kr  
 Plate: 34 row: H column: 10



## High quality sequence stop: 559.

FEATURES  
source

Location/Qualifiers

1..559

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="S21SNUS20-34-H10"

/sex="F"

/tissue\_type="Stomach"

/cell\_type="floating aggregates"

/lab\_host="SNU-520"

/lab\_host="Top10P"

/note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;

Site 2: NotI; The poly (A) + RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then deacapped

with tabacco acid pyrophosphatase (TAP). The deacapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10P by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 559;  
Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||||  
Db 118 GCATTGCCACTCCCATCTT 99

RESULT 19  
CF106297 586 bp mRNA linear EST 22-JUL-2003  
LOCUS CF106297/c  
DEFINITION IMAGE:6927543 5' similar to TR:Q9UDM7 Q9UDM7 KMGSC:H\_DJ0747618.5  
IMAGE:6927543 5' similar to TR:Q9UDM7 Q9UDM7 KMGSC:H\_DJ0747618.5  
PROTEIN ; mRNA sequence.  
CF106297  
ACCESSION CF106297.1 GI:33145364  
VERSION EST.  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 586)  
McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,  
Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,  
Ritter, E., Tsagaris, V., Runko, I., Maguire, L., Kennedy, S.,  
Bennett, V., Waterston, R. and Wilson, R.  
NIHNS Mouse  
Unpublished (2002)  
Contact: McCarrey/Eddy NIHNS Mouse

TITLE  
JOURNAL  
COMMENT

NIHNS Mouse  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

Library constructed and donated by J. McCarrey, Ph.D. (Southwest  
Foundation for Biomedical Research, Dept. of Genetics) - excision  
done by E.M. Eddy, Ph.D. (National Institutes of Health, National  
Institute of Environmental Health Sciences).  
MGI:2498328  
Seq primer: Primer name ambiguous.

FEATURES  
source

Location/Qualifiers

1..586

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CD-1"

/db\_xref="taxon:10090"

/clone="IMAGE:6927543"

/sex="male"

/tissue\_type="round spermatide, pooled from multiple mice"

/dev\_stage="60 day"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="McCarrey Eddy round spermatid"

/note="Organ: testis; Vector: pBluescript SK+

(Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo

dt-primed [5'-(GA)10-ACGACGCTGAGTTTCTTTT-3'] and

directionally cloned using 5' linkers 5'-ATTGCGACGAG-3'

and 5'-CTGTCGCG-3'. Size selection of &gt;400bp material

gives average insert size ranging from 1-2 kb. Library was

mass excised (from lambda-UniZAP-XR) and resulting

single-stranded phagemids were prepped and transformed

into DH10B. Library contains 98.5% recombinants.

References: J. Androl. 20:635-639 and Gene 25:263-269.

Library constructed and donated by J. McCarrey, Ph.D.  
(Southwest Foundation for Biomedical Research, Dept. of  
Genetics); excision done by E.M. Eddy, Ph.D. (National  
Institutes of Health, National Institute of Environmental  
Health Sciences). Original lambda-based library is  
available through ATCC, catalog #63423."

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 586;  
Best Local Similarity 100.0%; Pred. No. 0.38; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
|||||  
Db 108 GCATTGCCACTCCCATCTT 89

RESULT 20  
BG696693 590 bp mRNA linear EST 07-MAY-2001  
LOCUS BG696693/c  
DEFINITION 602659709F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4802594 5',  
IMAGE:4802594 5' similar to U00001.1  
mRNA sequence.  
BG696693  
ACCESSION BG696693.1 GI:13962102  
VERSION EST.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 590)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Straube, Ph.D.  
Email: cgabs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
plate: LLM10697 row: b column: 03  
High quality sequence stop: 590.

FEATURES  
source

Location/Qualifiers

1..590

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4802594"

/lab\_host="DH10B (T1 phage-resistant)"

ORIGIN  
 /clone\_lib="NCI\_CGAP\_Skn3"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI.  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

Query Match 100.0%; Score 20; DB 4; Length 590;  
 Best Local Similarity 100.0%; Pred. No. 0.38;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCATTGCCACTCCCATTTCTT 20  
 |||  
 Db 186 GCATTGCCACTCCCATTTCTT 167

RESULT 21  
 BP316675/c 592 bp mRNA linear EST 17-SEP-2004  
 LOCUS BP316675 Sugano cDNA library, pericardium Homo sapiens cDNA clone  
 DEFINITION PCDD01890, mRNA sequence.  
 ACCESSION BP316675  
 VERSION BP316675.1 GI:52245650  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
 1 (bases 1 to 592)  
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,  
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.  
 Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions

JOURNAL  
 COMMENT Department of Virology  
 Contact: Yutaka Suzuki  
 Genome Res. 14 (9), 1711-1718 (2004)  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp.  
 Location/Qualifiers

FEATURES  
 source  
 1..592  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="PCDD01890"  
 /rissue\_type="pericardium"  
 /clone\_lib="Sugano cDNA library, pericardium"

ORIGIN  
 Query Match 100.0%; Score 20; DB 5; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 0.38;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
 |||  
 Db 159 GCATTGCCACTCCCATTTCTT 140

RESULT 22  
 BP382116/c 615 bp mRNA linear EST 21-SEP-2004  
 LOCUS BP382116 Sugano cDNA library, adipose tissue Homo sapiens cDNA  
 DEFINITION BP382116  
 ACCESSION BP382116  
 VERSION BP382116.1 GI:52417687  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
 1 (bases 1 to 615)  
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,  
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.  
 Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions

TITLE  
 JOURNAL  
 COMMENT Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 Genome Res. 14 (9), 1711-1718 (2004)  
 Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp.  
 Location/Qualifiers

FEATURES  
 source  
 1..615  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="adSE01532"  
 /rissue\_type="adipose tissue"  
 /clone\_lib="Sugano cDNA library, adipose tissue"

ORIGIN  
 Query Match 100.0%; Score 20; DB 5; Length 615;  
 Best Local Similarity 100.0%; Pred. No. 0.38;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
 |||  
 Db 221 GCATTGCCACTCCCATTTCTT 202

RESULT 23  
 CK970536/c 621 bp mRNA linear EST 16-MAR-2004  
 LOCUS CK970536 BARC 9BOV Bos taurus cDNA clone 9BOV31\_D16 5', mRNA  
 DEFINITION 4086279 BARC 9BOV Bos taurus cDNA clone 9BOV31\_D16 5', mRNA  
 sequence.  
 ACCESSION CK970536  
 VERSION CK970536.1 GI:45488510  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE  
 AUTHORS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 621)  
 Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,  
 G.P., Bosak, S., Rubenfield, M. and Gabaree, L.C.  
 Production of EST from cDNA libraries derived from immunologically  
 activated bovine gut  
 Unpublished (2004)

JOURNAL  
 COMMENT Bovine Functional Genomics Laboratory  
 Contact: Tad S. Sonstegard  
 Animal and Natural Resources Institute  
 Belg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA  
 Tel: 3015048416  
 Fax: 3015048414  
 Email: tad@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred  
 0.000925 using options -trim\_alt "-trim\_fast. Vector identified  
 by cross\_match using options -mismatch 12 -minscore 12  
 Seq primer: CCCAGTCACGACGTGTGTAACG  
 High quality sequence stop: 621.  
 Location/Qualifiers

FEATURES  
 source  
 1..621  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /strain="Holstein"  
 /db\_xref="taxon:9913"  
 /clone="9BOV31\_D16"  
 /sex="Male"  
 /rissue\_type="pooled"  
 /dev\_stage="multiple"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="BARC 9BOV"  
 /note="Organ: Abomasum; Vector: pagen-1; Site: 1: EcoRV,  
 Site 2: NotI; Equimolar amounts of mRNA extracted from

fundic and pyloric abomasums of 18 and 21 week old steers.  
Exposure to *Ostertagia ostertagi* was initiated at 15 weeks  
of age. fundic and pyloric abomasum"

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 621;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCACTCCCATCTT 20  
|||||  
Db 510 GCATTGCCACTCCCATCTT 491

RESULT 24  
BG484381/c 625 bp mRNA linear EST 21-MAR-2001  
LOCUS 602505020F1 NIH\_MGC\_77 Homo sapiens CDNA clone IMAGE:4618421 5',  
DEFINITION mRNA sequence.

ACCESSION BG484381  
VERSION BG484381  
KEYWORDS GI:13416660  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 625)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: L10M1376 row: h column: 06  
High quality sequence stop: 624.  
Location/Qualifiers

## FEATURES

source

1..625  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4618421"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 77"  
/note="Organ: lung; Vector: pMDR-LIB (Clontech); Site 1:  
SfiI (ggcgccgcgcgc); Site 2: SfiI (ggccatcgcgc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGAGCGCGCATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 625;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCACTCCCATCTT 20  
|||||  
Db 438 GCATTGCCACTCCCATCTT 419

RESULT 25  
BF660115/c 631 bp mRNA linear EST 20-DEC-2000  
LOCUS BF660115

## DEFINITION

maa27g08.y1 NCI CGAP L110 Mus musculus CDNA clone IMAGE:3812534 5'  
similar to TR:Q9UDW7 Q9UDW7 WUGSC:H\_DJ0747G18.5 PROTEIN ;, mRNA  
sequence.

## ACCESSION

BF660115  
GI:11925249

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 631)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Other ESTs: maa27g08.x1  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>

JOURNAL  
COMMENTFEATURES  
source

MGI:1454646  
Seq primer: -40RP from Glbco  
High quality sequence stop: 437.  
Location/Qualifiers  
1..631  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3812534"  
/sex="female"  
/dev stage="10 weeks"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP L110"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.6 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 631;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATTGCCACTCCCATCTT 20  
|||||  
Db 240 GCATTGCCACTCCCATCTT 221

## RESULT 26

## CA535709/c

LOCUS CA535709 632 bp mRNA linear EST 18-NOV-2002  
DEFINITION C0223B02-5N NIA Mouse 7.5-dpc whole Embryo CDNA Library (Long) Mus  
musculus CDNA clone NIA: C0223B02 IMAGE:30012781 5', mRNA sequence.

ACCESSION CA535709  
VERSION CA535709.1 GI:25069331  
EST.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 632)  
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Tanaka, T., Lim, M.K.,  
Luo, A., and Ko, M.S.H. Systematic Analyses of NIA Mouse 7.5-dpc whole Embryo CDNA Library  
(Long)  
Unpublished (2001)  
Contact: Dawood B. Dudekula

JOURNAL  
COMMENT

Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@gsun-grc.nia.nih.gov  
Plate: C0223 row: B column: 02  
Seq primer: M13 Reverse  
High quality sequence stop: 632  
POLYA=No.

# FEATURES

## SOURCE

Location/Qualifiers  
1..632  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/db\_xref="taxon:10090"  
/clone="NIA:C0223B02 IMAGE:30012781"  
/tissue\_type="whole embryo including extraembryonic  
tissues at 7.5-days postcoitum"  
/dev\_stage="7.5-days postcoitum"  
/lab\_host="DH10B"  
/clone\_id="NIA Mouse 7.5-dpc Whole Embryo cDNA Library  
(Long)"  
/note="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://gsun-grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). (PMID: 11544199)). Total RNAs were  
extracted from a pool of four embryos at 7.5-days  
postcoitum. Double-stranded cDNAs were synthesized with an  
Oligo(dT) primer (Invitrogen):  
5'-pGAGTGTCTAGATCGGCGCGCCCTTTTCTTTTCTTTT-3' from  
7 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to Loe-linker L-SalI, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer SalI-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.2 kb. The library was constructed  
by Yulan Piao (NIA)."

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 632;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCATCCCATCTT 20  
|||||  
Db 455 GCATTGCCATCCCATCTT 436

RESULT 27  
LOCUS CB267111 646 bp mRNA linear EST 20-FEB-2003  
DEFINITION 1006017 Human Fat Cell 5'-stretch plus cDNA Library Homo sapiens  
ACCESSION CB267111  
VERSION CB267111.1 GI:28441697  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 646)  
AUTHORS Yang, R.-Z., Shuldiner, A. and Gong, D.-W.  
TITLE EST analysis of human adipose gene expression  
JOURNAL Unpublished (2002)  
COMMENT Contact: Gong Da-Wei

Division of Endocrinology, Diabetes and Nutrition  
University of Maryland  
660 Redwood St., HH497, Baltimore, MD 21201, USA  
Tel: 410 706 1672  
Fax: 410 706 1622  
Email: dgong@medicine.umaryland.edu  
PCR Primers  
FORWARD: CTCGGAGAGCGCCCATTTGTTGGT  
BACKWARD: AATGCACTCATATAGCGCAATTGG  
Seq primer: GTTGTACCGCGAATTC.

# FEATURES

## SOURCE

Location/Qualifiers  
1..646  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/sex="Male and Female"  
/tissue\_type="Adipose"  
/clone\_id="Human Fat Cell 5'-stretch plus cDNA Library"  
/note="Vector: lambdaTriplex"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 646;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCATCCCATCTT 20  
|||||  
Db 223 GCATTGCCATCCCATCTT 204

RESULT 28  
LOCUS B1144404 653 bp mRNA linear EST 05-JUL-2001  
DEFINITION 60290854BP1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5049851 5',  
mRNA sequence.  
ACCESSION B1144404  
VERSION B1144404.1 GI:14604405  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus (house mouse)  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 653)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L14M1115 row: P column: 12  
High quality sequence stop: 653.

# FEATURES

## SOURCE

Location/Qualifiers  
1..653  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5049851"  
/lab\_host="NCI CGAP L19"  
/clone\_id="NCI CGAP L19"  
/note="Organ: Liver; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 653;

Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTGCCACTCCCATCTT 20  
|||||  
DB 507 GCATTGCCACTCCCATCTT 488

RESULT 29  
BI908609/c 663 bp mRNA linear EST 16-OCT-2001  
LOCUS 603066720P1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5215900 5',  
DEFINITION mRNA sequence.  
ACCESSION BI908609  
VERSION BI908609.1 GI:16171624  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 663)  
NIH-MGC http://mgs.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov

Plate: LLM9443 row: g column: 05  
High quality sequence stop: 663.  
Location/Qualifiers

## FEATURES

1..663  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5215900"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/clone\_id="NIH\_MGC\_118"  
/note="Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 663;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTGCCACTCCCATCTT 20  
|||||  
DB 537 GCATTGCCACTCCCATCTT 518

RESULT 30  
BF237046/c 677 bp mRNA linear EST 14-NOV-2000  
LOCUS 607026681P1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4161717 5',  
DEFINITION mRNA sequence.  
ACCESSION BF237046  
VERSION BF237046.1 GI:11150963  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 677)  
NIH-MGC http://mgs.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov

Plate: LLM9443 row: b column: 22  
High quality sequence stop: 673.  
Location/Qualifiers

## FEATURES

1..677  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4161717"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_id="NCI\_CGAP\_L19"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTGCCACTCCCATCTT 20  
|||||  
DB 342 GCATTGCCACTCCCATCTT 323

RESULT 31  
BF236900/c 698 bp mRNA linear EST 14-NOV-2000  
LOCUS 602026519P1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4161773 5',  
DEFINITION mRNA sequence.  
ACCESSION BF236900  
VERSION BF236900.1 GI:11150817  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 698)  
NIH-MGC http://mgs.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov

Plate: LLM9443 row: e column: 06  
High quality sequence stop: 691.  
Location/Qualifiers

## FEATURES

1..698  
/organism="Mus musculus"  
/mol\_type="mRNA"

/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:416173"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP Lib"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI CGAP library."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 698;  
Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTTCTT 20  
Db 465 GCATTGCCACTCCCATTTCTT 446

RESULT 32  
BI332607/c 710 bp mRNA linear EST 30-JUL-2001  
LOCUS 602980747F1 NCI CGAP\_L19 Mus musculus cDNA clone IMAGE:5133874 5',  
DEFINITION mRNA sequence.

ACCESSION BI332607  
VERSION BI332607.1 GI:15017264  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Plate: LHAM1328 row: m column: 11  
High quality sequence start: 8  
High quality sequence stop: 701.

FEATURES Location/Qualifiers

1..710  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5133874"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP Lib"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI CGAP library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 710;  
Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTTCTT 20  
Db 496 GCATTGCCACTCCCATTTCTT 477

RESULT 33

BI915586/c

BI915586 718 bp mRNA linear EST 16-OCT-2001  
LOCUS 603176945F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5241299 5',  
DEFINITION mRNA sequence.

ACCESSION BI915586  
VERSION BI915586.1 GI:16199311  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Plate: LHAM1608 row: 1 column: 12  
High quality sequence stop: 716.

FEATURES Location/Qualifiers

1..718  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5241299"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_121"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: EcoRV (destroyed); RNA source anonymous pool of  
fetal brains, female age 20 weeks, female age 24 weeks,  
and male age 26 weeks. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
0.7-3.5 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 017. Note:  
this is a NIH\_MGC library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 718;  
Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTTCTT 20  
Db 708 GCATTGCCACTCCCATTTCTT 689

RESULT 34

BG695886 732 bp mRNA linear EST 07-MAY-2001  
LOCUS 602657850F1 NCI CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4800708 5',  
DEFINITION mRNA sequence.

ACCESSION BG695886  
VERSION BG695886.1 GI:13960469  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L14M10692 row: c column: 13  
High quality sequence stop: 732.  
Location/Qualifiers

## FEATURES

SOURCE

1..732

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4800708"

/lab\_host="DH10B (TI phage-resistant)"

/clone\_1lb="NCI\_CGAP\_Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6, Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI\_CGAP library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 732;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GCATTGCCACTCCCATCTT 20

Db

177 GCATTGCCACTCCCATCTT 158

## RESULT 35

BG194285/c 743 bp mRNA linear EST 21-APR-2001  
LOCUS BG194285  
DEFINITION RS113430 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG194285  
VERSION BG194285.1 GI:13715972  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 743)  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kikka, A., Hees, D., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.  
Creation of genome-wide protein expression libraries using random activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)

## REFERENCE

AUTHORS Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kikka, A., Hees, D., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.  
Creation of genome-wide protein expression libraries using random activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)

## TITLE

JOURNAL MEDLINE  
PUBMED 11329013  
Contact: Scott J. Cain  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: [scain@atherys.com](mailto:scain@atherys.com)  
High quality sequence stop: 551.  
Location/Qualifiers

## COMMENT

Atherys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: [scain@atherys.com](mailto:scain@atherys.com)  
High quality sequence stop: 551.  
Location/Qualifiers

## FEATURES

1..743  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_1lb="NCI\_CGAP\_Skn3"  
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."

Query Match 100.0%; Score 20; DB 4; Length 743;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GCATTGCCACTCCCATCTT 20

Db

249 GCATTGCCACTCCCATCTT 230

## RESULT 36

BG695953/c 743 bp mRNA linear EST 07-MAY-2001  
LOCUS BG695953  
DEFINITION 602657968F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4800809 5', mRNA sequence.  
ACCESSION BG695953  
VERSION BG695953.1 GI:13960591  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 743)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L14M10692 row: g column: 18  
High quality sequence stop: 731.  
Location/Qualifiers

## REFERENCE

AUTHORS Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kikka, A., Hees, D., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.  
Creation of genome-wide protein expression libraries using random activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)

## TITLE

JOURNAL MEDLINE  
PUBMED 11329013  
Contact: Scott J. Cain  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: [scain@atherys.com](mailto:scain@atherys.com)  
High quality sequence stop: 551.  
Location/Qualifiers

## FEATURES

1..743  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4800809"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_1lb="NCI\_CGAP\_Skn3"  
/note="Organ: skin; Vector: pCMV-SPORT6, Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI\_CGAP library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 743;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GCATTGCCACTCCCATCTT 20

Db

251 GCATTGCCACTCCCATCTT 232

## RESULT 37

CR383515/c 747 bp mRNA linear EST 04-MAY-2004  
LOCUS CR383515  
DEFINITION CR383515 Bovine multi-stage muscle library (bca5) Bos taurus cDNA clone bcaj0001a.d.01 5prim, mRNA sequence.  
ACCESSION CR383515  
VERSION CR383515.1 GI:47005419  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 747)  
Chevalier, C  
AGENAE; a French Animal Genome project  
JOURNAL  
Unpublished (2004)  
COMMENT  
Contact: Martin P  
INRA, Genomique & Physiologie de la Lactation  
Domaine de Vilvert, 78352 JOUY-EN-JOSAS cedex, FRANCE  
Tel: +33 (0) 1.34.65.25.82  
Fax: +33 (0) 1.34.65.29.26  
Email: Patrice.Martin@jouy.inra.fr  
Sequence cleaned of vector, adaptor and repetitions. Contact us  
at bigenaproj@jouy.inra.fr to obtain the chromatogram of this  
sequence.

Plate: 0001 row: d column: 1.  
Location/Qualifiers

#### FEATURES

source

1..747  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="bcaj0001a.d.01"  
/tissue\_type="muscles : heart, longissimus thoracis,  
semitendinosus, masseter, cutaneous trunci"  
/dev\_strage="from embryos to adults"  
/clone\_id="Bovine multi-stage muscles library (bcaj)"  
/note="Clone distribution : AGENAE Resource centre.  
Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA  
Radiobiologie et Etude du genome (LREG), Domaine de  
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0)  
1.34.65.28.02, +33 (0) 1.34.65.22.73"

#### ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 747;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCATTGCCACTCCCATCTT 20  
Db 416 GCATTGCCACTCCCATCTT 397

RESULT 38 762 bp mRNA linear EST 23-JAN-2001  
BF980113  
LOCUS 602288115T1 NIH\_MGC\_97 Homo sapiens CDNA clone IMAGE:4373955 3'  
DEFINITION mRNA sequence.  
ACCESSION BF980113 GI:12347328  
VERSION BF980113  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 762)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Plate: LLM10036 row: n column: 04  
High quality sequence start: 25  
High quality sequence stop: 752.  
Location/Qualifiers  
1..762

#### FEATURES

source

#### ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 762;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATCTT 20  
Db 543 GCATTGCCACTCCCATCTT 562

RESULT 39 776 bp mRNA linear EST 15-MAY-2001  
BG739895  
LOCUS 60230838F1 NCI\_CGAP\_Skn3 Homo sapiens CDNA clone IMAGE:4776320 5'  
DEFINITION mRNA sequence.  
ACCESSION BG739895  
VERSION BG739895.1 GI:14050548  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 776)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM10628 row: k column: 09  
High quality sequence stop: 776.  
Location/Qualifiers

#### FEATURES

source

1..776  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4776320"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_id="NCI CGAP\_Skn3"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP library."

#### ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 776;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCATTGCCACTCCCATCTT 20



Db 87 GCATTGCCACTCCCATCTT 68

|||||

RESULT 40  
BG697487 781 bp mRNA linear EST 07-MAY-2001  
LOCUS 602660680F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4804074 5',  
DEFINITION mRNA sequence.  
ACCESSION BG697487.1 GI:13963760  
VERSION BG697487.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 781)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM10700 row: 0 column: 19  
High quality sequence stop: 781.  
Location/Qualifiers  
1..781  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4804074"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP Skn3"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: Nci1;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 781;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
|||||

Db 361 GCATTGCCACTCCCATCTT 342

RESULT 41  
BG189090 789 bp mRNA linear EST 21-APR-2001  
LOCUS RST8128 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG189090  
VERSION BG189090.1 GI:13710777  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 789)  
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,  
Whitington,J., Lerner,L., Costanzo,D., McElligott,K., Boozey,S.,  
Mays,R., Smith,E., Veloso,N., Kilka,A., Hess,J., Cochren,K., Lo,K.,  
Offenbacher,J., Danzig,J. and Ducar,M.  
TITLE Creation of genome-wide protein expression libraries using random  
activation of gene expression

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
MEDLINE 21227151  
PUBMED 11329013  
COMMENT Contact: Scott J. Cain  
Atherys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atherys.com  
High quality sequence stop: 556.  
Location/Qualifiers  
1..789  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="HT1080"  
/clone\_lib="Atherys RAGE Library"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 789;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATCTT 20  
|||||

Db 279 GCATTGCCACTCCCATCTT 260

RESULT 42  
BG212376 800 bp mRNA linear EST 21-APR-2001  
LOCUS RST31963 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.  
DEFINITION BG212376  
ACCESSION BG212376  
VERSION BG212376.1 GI:13734063  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 800)  
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,  
Whitington,J., Lerner,L., Costanzo,D., McElligott,K., Boozey,S.,  
Mays,R., Smith,E., Veloso,N., Kilka,A., Hess,J., Cochren,K., Lo,K.,  
Offenbacher,J., Danzig,J. and Ducar,M.  
TITLE Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
JOURNAL 21227151  
MEDLINE 11329013  
PUBMED  
COMMENT Contact: Scott J. Cain  
Atherys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atherys.com  
High quality sequence stop: 408.  
Location/Qualifiers  
1..800  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="HT1080"  
/clone\_lib="Atherys RAGE Library"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

FEATURES  
source

cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 800;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTCCCATTTCTT 20  
|||||  
Db 271 GCATTGCCACTCCCATTTCTT 252

RESULT 43  
BG865428/c 800 bp mRNA linear EST 29-MAY-2001  
DEFINITION 602783545F1 NCI\_CGAP\_SG2 Mus musculus cDNA clone IMAGE:4909906 5',  
mRNA sequence.  
ACCESSION BG865428 GI:14215968  
VERSION BG865428.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 800)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL0809 row: 1 column: 11  
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Location/Qualifiers  
1. 800

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Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

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QY 1 GCATTGCCACTCCCATTTCTT 20  
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mRNA sequence.  
ACCESSION BI247050  
VERSION BI247050.1 GI:14791603  
KEYWORDS EST.

## SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 809)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL1308 row: m column: 21  
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Location/Qualifiers  
1. 809

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENTFEATURES  
source

/organism="Mus musculus"  
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Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

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RESULT 45  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BUS41989 816 bp mRNA linear EST 13-SEP-2002  
AGENCOURT 10252853 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6573777  
BUS41989  
BUS41989.1 GI:22852472  
EST.  
Homo sapiens (human)  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 816)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
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Location/Qualifiers  
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FEATURES  
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Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH_MGC library."
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## ORIGIN

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